

From: Schnizer, Richard
Sent: Friday, September 09, 2005 3:33 PM
To: STIC-Biotech/ChemLib
Subject: 10/622,108

Please search SEQ ID NOS: 2 and 28-30 from 10/622,108.

Note that SEQ ID NO:28 is (GGGGS)₂, SEQ ID NO:29 is (GGGGS)₃, and SEQ ID NO:30 is (GGGGS)₄.
A search of SEQ ID NO:30 will probably get SEQ ID NOS: 28 and 29, unless there are too many hits.

SEQ ID NOS: 28-30 are claimed in a form linking an interferon alpha molecule to the N-terminus of an Ig heavy chain.

Thank you-

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Patent Examiner
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9-19
Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:22:24 ; Search time 124.444 Seconds
(without alignments)
65.078 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGSGGGGGGGGGGGGGGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 525249

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	20	9	US-09-953-321-12
2	112	100.0	20	10	US-09-910-483-96
3	112	100.0	20	10	US-09-967-237-116
4	112	100.0	20	10	US-09-911-261A-21
5	112	100.0	20	10	US-09-969-748C-39
6	112	100.0	20	10	US-09-949-039-57
7	112	100.0	20	14	US-10-112-612-75
8	112	100.0	20	14	US-10-057-408-21
9	112	100.0	20	14	US-10-021-818-7
10	112	100.0	20	14	US-10-072-301-4
11	112	100.0	20	14	US-10-071-866-4
					Sequence 12, Appl
					Sequence 96, Appl
					Sequence 116, Appl
					Sequence 21, Appl
					Sequence 39, Appl
					Sequence 57, Appl
					Sequence 75, Appl
					Sequence 21, Appl
					Sequence 7, Appl
					Sequence 4, Appl

12	112	100.0	20	14	US-10-112-691-75	Sequence 75, Appl
13	112	100.0	20	14	US-10-287-941-1	Sequence 1, Appl
14	112	100.0	20	15	US-10-360-828-4	Sequence 4, Appl
15	112	100.0	20	15	US-10-032-037B-123	Sequence 123, App
16	112	100.0	20	15	US-10-029-988B-123	Sequence 123, App
17	112	100.0	20	15	US-10-032-423A-123	Sequence 123, App
18	112	100.0	20	15	US-10-622-108-30	Sequence 30, Appl
19	112	100.0	20	15	US-10-029-926B-123	Sequence 123, App
20	112	100.0	20	15	US-10-333-487-21	Sequence 21, Appl
21	112	100.0	20	16	US-10-475-540-9	Sequence 9, Appl
22	112	100.0	20	16	US-10-334-235-20	Sequence 20, Appl
23	112	100.0	20	16	US-10-746-149-29	Sequence 29, Appl
24	112	100.0	20	16	US-10-609-019-8	Sequence 8, Appl
25	112	100.0	20	16	US-10-470-987-20	Sequence 20, Appl
26	112	100.0	20	16	US-10-746-943-84	Sequence 84, Appl
27	112	100.0	20	16	US-10-492-729-16	Sequence 16, Appl
28	112	100.0	20	16	US-10-634-740-20	Sequence 20, Appl
29	112	100.0	20	17	US-10-885-225-149	Sequence 149, App
30	112	100.0	20	17	US-10-792-498-31	Sequence 31, Appl
31	112	100.0	20	17	US-10-770-304-5	Sequence 5, Appl
32	112	100.0	20	17	US-10-506-651-20	Sequence 20, Appl
33	112	100.0	20	17	US-10-954-094-149	Sequence 149, App
34	112	100.0	20	18	US-10-988-485-4	Sequence 4, Appl
35	112	100.0	20	18	US-10-792-682-75	Sequence 75, Appl
36	112	100.0	20	18	US-10-787-219A-48	Sequence 48, Appl
37	112	100.0	24	9	US-09-851-271A-12	Sequence 12, Appl
38	112	100.0	24	16	US-10-769-831-17	Sequence 17, Appl
39	112	100.0	24	17	US-10-770-140-17	Sequence 17, Appl
40	112	100.0	25	10	US-09-969-748C-40	Sequence 40, Appl
41	112	100.0	25	10	US-09-949-039-56	Sequence 56, Appl
42	112	100.0	25	13	US-10-081-281-32	Sequence 32, Appl
43	112	100.0	25	14	US-10-013-173-11	Sequence 11, Appl
44	112	100.0	25	14	US-10-150-762-11	Sequence 11, Appl
45	112	100.0	25	14	US-10-244-821-11	Sequence 11, Appl
46	112	100.0	25	14	US-10-261-798-91	Sequence 91, Appl
47	112	100.0	25	16	US-10-769-831-16	Sequence 16, Appl
48	112	100.0	25	16	US-10-634-740-21	Sequence 21, Appl
49	112	100.0	25	17	US-10-770-140-1	Sequence 1, Appl
50	112	100.0	25	17	US-10-770-140-16	Sequence 16, Appl
51	112	100.0	25	17	US-10-770-304-4	Sequence 4, Appl
52	112	100.0	25	17	US-10-506-651-14	Sequence 14, Appl
53	112	100.0	26	16	US-10-646-308-36	Sequence 36, Appl
54	112	100.0	30	10	US-09-833-203-19	Sequence 19, Appl
55	112	100.0	30	16	US-10-492-729-17	Sequence 17, Appl
56	112	100.0	30	16	US-10-634-740-22	Sequence 22, Appl
57	112	100.0	30	17	US-10-792-498-32	Sequence 32, Appl
58	112	100.0	35	14	US-10-013-173-30	Sequence 30, Appl
59	112	100.0	35	14	US-10-150-762-30	Sequence 30, Appl
60	112	100.0	35	14	US-10-244-821-30	Sequence 30, Appl
61	112	100.0	40	13	US-10-081-400-1	Sequence 1, Appl
62	112	100.0	40	13	US-10-005-438-9	Sequence 9, Appl
63	112	100.0	40	15	US-10-257-864A-137	Sequence 137, App
64	112	100.0	40	15	US-10-257-864A-138	Sequence 138, App
65	112	100.0	40	16	US-10-608-710-6	Sequence 6, Appl
66	112	100.0	40	16	US-10-768-873-1	Sequence 1, Appl
67	112	100.0	40	16	US-10-399-585-176	Sequence 176, App
68	112	100.0	40	16	US-10-399-585-177	Sequence 177, App
69	112	100.0	40	16	US-10-645-085A-137	Sequence 137, App
70	112	100.0	40	16	US-10-645-085A-138	Sequence 138, App
71	112	100.0	40	16	US-10-492-729-18	Sequence 18, Appl
72	112	100.0	40	17	US-10-917-899-9	Sequence 9, Appl
73	112	100.0	40	17	US-10-792-498-33	Sequence 33, Appl
74	112	100.0	40	20	US-11-016-189-1	Sequence 1, Appl
75	112	100.0	40	20	US-11-049-853-1	Sequence 1, Appl
76	112	100.0	50	10	US-09-949-039-32	Sequence 32, Appl
77	112	100.0	50	17	US-10-842-054-15	Sequence 15, Appl
78	112	100.0	50	17	US-10-792-498-34	Sequence 34, Appl
79	112	100.0	50	18	US-10-841-819B-31	Sequence 31, Appl
80	108	96.4	20	13	US-10-081-400-3	Sequence 3, Appl
81	108	96.4	20	13	US-10-074-956-18	Sequence 18, Appl
82	108	96.4	20	14	US-10-077-213-3	Sequence 3, Appl
83	108	96.4	20	14	US-10-077-210-3	Sequence 3, Appl
84	108	96.4	20	15	US-10-399-518-182	Sequence 182, App

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:14:03 ; Search time 118.667 Seconds
(without alignments)
86.305 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGGGGGGGGGGGGGGGGGGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	73.2	25	2	Q42086 arabidopsis
2	80	71.4	28	2	Q37931 bacterioph
3	80	71.4	36	2	Q02023 lycopersico
4	80	71.4	43	1	GRW1_LYCES
5	79	70.5	42	2	Q23471 arabidopsis
6	77	68.8	49	2	P93517 zea mays (m
7	75	67.0	47	2	Q9S857 glycine max
8	72	64.3	15	2	Q9S8K3 glycine max
9	70	62.5	43	2	Q8QUM1 infectious
10	67	59.8	34	2	Q7M322 fasciola he
11	66	58.9	45	2	Q7R2M4 neurospora
12	62	55.4	46	2	Q708X1 cicier ariet
13	61	54.5	27	1	FBRL PHYPO
14	60.5	54.0	48	2	Q60413 cricetus cr
15	60	53.6	43	2	Q63281 rattus norv
16	59	52.7	26	2	Q42226 arabidopsis
17	59	52.7	50	2	Q94319 oryza sativ
18	57.5	51.3	36	2	Q6X920 equus cabal
19	57.5	51.3	50	2	Q6K325 oryza sativ
20	57	50.9	45	1	YD27_HAEIN
21	57	50.9	50	2	Q8N008 plasmodium
22	57	50.9	50	2	Q8N009 plasmodium
23	56	50.0	47	2	Q73CB1 bacillus ce
24	56	50.0	50	2	Q73CM9 bacillus ce
25	55	49.1	40	2	Q9BDE8 sus scrofa
26	54	48.2	20	2	Q9UR60 candida alb
27	54	48.2	31	1	FBRL RAT
28	54	48.2	41	2	Q9TVQ8 rattus norv
29	54	48.2	43	2	Q65183 bacillus li
30	54	48.2	50	2	Q7X187 oryza sativ
31	53.5	47.8	49	2	Q62BA3 bacillus li

32	53	47.3	47	2	Q81U37	Q81U37 bacillus an
33	53	47.3	50	2	Q81UD0	Q81UD0 bacillus an
34	52.5	46.9	50	1	YKQ5_CABEL	P34300 caenorhabdi
35	50.5	45.1	34	2	Q8J0A0	Q8J0A0 arthroderma
36	50.5	45.1	34	2	Q8J1L7	Q8J1L7 trichophyto
37	50	44.6	33	2	Q17071	Q17071 anthraaea p
38	50	44.6	35	2	Q6F345	Q6F345 oryza sativ
39	49	43.8	22	2	Q6V0X7	Q6V0X7 serratia ma
40	48	42.9	22	2	Q17072	Q17072 anthraaea p
41	48	42.9	23	2	Q6LC06	Q6LC06 homo sapien
42	48	42.9	40	2	Q8ERB7	Q8ERB7 oceanobacil
43	48	42.9	50	2	Q9N120	Q9N120 plasmodium
44	47.5	42.4	35	2	Q64L91	Q64L91 gulo gulo (
45	47.5	42.4	47	2	Q8N010	Q8N010 plasmodium
46	47	42.0	41	2	Q9TNZ5	Q9TNZ5 rattus norv
47	47	42.0	41	2	Q99PH5	Q99PH5 mus musculu
48	47	42.0	44	2	Q95562	Q95562 rattus norv
49	47	42.0	49	1	YKQ6_CABEL	P34301 caenorhabdi
50	46.5	41.5	50	1	YKQ2_CABEL	P34297 caenorhabdi
51	46	41.1	20	2	Q81Z13	Q81Z13 homo sapien
52	46	41.1	42	2	Q8MXU9	Q8MXU9 caenorhabdi
53	46	41.1	44	2	Q9Y199	Q9Y199 cyprinus ca
54	46	41.1	45	2	Q7XMY7	Q7XMY7 oryza sativ
55	45	40.2	21	2	Q9R204	Q9R204 mus musculu
56	45	40.2	34	2	Q9A4N0	Q9A4N0 caulobacter
57	45	40.2	40	2	Q65SK6	Q65SK6 manheimia
58	45	40.2	46	2	Q6MM16	Q6MM16 bdellovibri
59	45	40.2	46	2	Q81NP8	Q81NP8 bacillus an
60	45	40.2	50	2	Q8XY14	Q8XY14 ralstonia s
61	44.5	39.7	46	2	Q6A186	Q6A186 cryptospori
62	44	39.3	35	2	Q94214	Q94214 oryza sativ
63	44	39.3	48	2	Q8YUR2	Q8YUR2 anabaena sp
64	43	38.4	20	2	Q7JMY8	Q7JMY8 leishmania
65	43	38.4	20	2	Q8W238	Q8W238 glycine max
66	43	38.4	34	2	Q6VV38	Q6VV38 human herpe
67	43	38.4	48	2	Q6JDL2	Q6JDL2 canis famil
68	42	37.5	47	2	Q9XXD3	Q9XXD3 caenorhabdi
69	42	37.5	48	2	Q7DNB6	Q7DNB6 oryza sativ
70	42	37.5	48	2	Q84DW9	Q84DW9 tropheryma
71	42	37.5	49	2	Q9SCS1	Q9SCS1 arabidopsis
72	41	36.6	16	2	Q7JNE8	Q7JNE8 drosophila
73	41	36.6	17	1	H4_SEPOF	Q7M325 sepiia offic
74	41	36.6	20	2	Q7M3Z6	Q7M3Z6 hemocentrot
75	41	36.6	23	2	Q7M3Q9	Q7M3Q9 fasciola he
76	41	36.6	23	2	Q9TWK2	Q9TWK2 mytilus edu
77	41	36.6	23	2	P70093	P70093 xenopus lae
78	41	36.6	24	1	H4_MEDSA	P62789 medicago sa
79	41	36.6	33	2	Q27637	Q27637 drosophila
80	41	36.6	34	2	Q27821	Q27821 trichomonas
81	41	36.6	34	2	Q6VV39	Q6VV39 human herpe
82	41	36.6	35	2	Q27754	Q27754 pisaster oc
83	41	36.6	41	2	Q71ZB3	Q71ZB3 anolis caro
84	41	36.6	50	2	Q4YVS5	Q4YVS5 oryza sativ
85	40.5	36.2	50	1	VG38_BPM2	Q64329 mycobacteri
86	40	35.7	27	2	Q9XJ05	Q9XJ05 oryza sativ
87	40	35.7	34	2	Q6VV29	Q6VV29 human herpe
88	40	35.7	42	2	Q9PWJ2	Q9PWJ2 cyprinus ca
89	40	35.7	44	2	Q6Y1D5	Q6Y1D5 lactuca sat
90	40	35.7	46	2	Q75MQ8	Q75MQ8 homo sapien
91	40	35.7	49	2	Q7VCB8	Q7VCB8 prochloroco
92	39.5	35.3	37	2	Q7X9E6	Q7X9E6 phaseolus v
93	39	34.8	23	2	Q9UC00	Q9UC00 homo sapien
94	39	34.8	38	1	CU47_LACCU	Q9TVM6 ichtyophth
95	39	34.8	38	1	CU47_LACCU	P80323 lactobacill
96	39	34.8	44	2	Q848N1	Q848N1 uncultured
97	39	34.8	48	2	Q7KJTB	Q7KJTB plasmodium
98	39	34.8	48	2	Q9N6A3	Q9N6A3 plasmodium
99	38	33.9	26	2	O22463	Q22463 hordeum vul
100	38	33.9	36	2	Q7RSC3	Q7RSC3 plasmodium

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:15:03 ; Search time 25.3333 Seconds
(without alignments)
75.961 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGGGGGGGGGGGGGGGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	79	70.5	42	A71429	hypothetical prote
2	77	68.8	49	T02026	glycine-rich prote
3	67	59.8	34	A61184	presclerotized egg
4	61	54.5	27	A31508	34K nucleolar prot
5	57	50.9	45	A64026	hypothetical prote
6	54	48.2	31	A23887	fibrillar - rat
7	53	47.3	29	S06854	chorion class B pr
8	52.5	46.9	50	C88533	hypothetical prote
9	52	46.4	12	A58375	microcin B17 - Esc
10	47	42.0	49	D88533	5.0K hypothetical
11	45	40.2	34	H87595	hypothetical prote
12	44	39.3	48	A52090	hypothetical prote
13	42	37.5	47	T26981	hypothetical prote
14	42	37.5	49	T46085	hypothetical prote
15	41	36.6	17	B61321	histone H4 - chick
16	41	36.6	17	A61321	histone H4 - commo
17	41	36.6	20	S68620	histone H4 - sea u
18	41	36.6	23	I51431	histone H4-1 precu
19	41	36.6	23	A32473	histidine-rich pro
20	41	36.6	24	B43295	histone H4 - alfal
21	41	36.6	35	A29663	histone H4 - starf
22	41	36.6	41	A58213	protamine - green
23	40.5	36.2	50	D72804	gp38 protein - Myc
24	38	33.9	26	T04371	thauartin-like pro
25	38	33.9	47	A61384	tracheal mucin gly
26	37.5	33.5	35	A61375	basic fibroblast g
27	37.5	33.5	49	T48681	185 kDa glycophosp
28	36	32.1	39	T12912	hypothetical prote
29	35	31.2	10	F60527	sperm-activating p

30	35	31.2	31	2	S10260	histone H4.2 - Tet
31	35	31.2	31	2	S10262	histone H4.2 - Tet
32	35	31.2	31	2	S10264	histone H4.2 - Tet
33	35	31.2	31	2	S10266	histone H4.2 - Tet
34	35	31.2	31	2	S10268	histone H4.2 - Tet
35	35	31.2	31	2	S10270	histone H4.2 - Tet
36	35	31.2	31	2	S10272	histone H4.2 - Tet
37	35	31.2	31	2	S10274	histone H4.2 - Tet
38	35	31.2	31	2	S10276	histone H4.2 - Tet
39	35	31.2	31	2	S10278	histone H4.2 - Tet
40	35	31.2	31	2	S10280	histone H4.2 - Tet
41	35	31.2	31	2	S10282	histone H4.2 - Tet
42	35	31.2	31	2	S10284	histone H4.2 - Tet
43	35	31.2	31	2	S10286	histone H4.2 - Tet
44	35	31.2	31	2	S10288	histone H4.2 - Tet
45	35	31.2	31	2	S10292	histone H4.2 - Tet
46	35	31.2	31	2	S10294	histone H4.2 - Tet
47	35	31.2	31	2	S10296	histone H4.2 - Tet
48	35	31.2	31	2	S10298	histone H4.2 - Tet
49	35	31.2	31	2	S10300	histone H4.2 - Tet
50	35	31.2	32	2	S12150	histone H4.2 - Gla
51	35	31.2	40	2	P00202	endo-1,4-beta-xyla
52	35	31.2	42	2	A99578	lipoprotein vsah l
53	34	30.4	15	2	S62609	glutathione-disulf
54	34	30.4	38	2	B36207	hypothetical prote
55	33	29.5	15	2	E56978	collagen alpha 2(X
56	33	29.5	22	2	C42856	hypothetical prote
57	33	29.5	34	2	A58996	peptidylprolyl iso
58	33	29.5	50	2	AC2221	hypothetical prote
59	32	28.6	17	2	PH0757	T-cell receptor be
60	32	28.6	19	2	PT0332	ig heavy chain CRD
61	32	28.6	28	2	P00263	dnak-type molecula
62	32	28.6	40	2	C38578	protein kinase 3 (
63	32	28.6	48	2	P82015	hypothetical prote
64	31	27.7	31	2	S10230	histone H4.2 - Tet
65	31	27.7	44	2	B39859	flavocytochrome c
66	30	26.8	13	1	JTJG3	tremerogen a-13 -
67	30	26.8	13	2	S48210	collagen alpha 1(V
68	30	26.8	24	2	S53749	histone H4 - rat
69	30	26.8	30	2	A34874	transforming prote
70	30	26.8	33	2	PC2055	lectin - cornucopi
71	30	26.8	33	2	S69595	gene 4f-rnp protei
72	30	26.8	34	2	T36735	hypothetical prote
73	30	26.8	35	2	T04151	probable 1-aminocy
74	30	26.8	38	2	S15845	cathepsin L (EC 3.
75	30	26.8	39	2	B95063	hypothetical prote
76	30	26.8	46	2	A45758	hypothetical gluco
77	30	26.8	49	2	S46908	cell division prot
78	30	26.8	50	2	S77924	2,4-dichlorophenol
79	30	26.8	50	2	AG3298	hypothetical prote
80	29	25.9	10	2	B60588	sperm-activating p
81	29	25.9	10	2	C60588	sperm-activating p
82	29	25.9	10	2	C60527	sperm-activating p
83	29	25.9	10	2	E60527	sperm-activating p
84	29	25.9	10	2	B60788	sperm-activating p
85	29	25.9	10	2	B60589	sperm-activating p
86	29	25.9	16	2	A44897	ferredoxin-NADP re
87	29	25.9	18	2	B32473	histidine-rich pro
88	29	25.9	29	2	S08555	ribosomal protein
89	29	25.9	29	2	B43553	hypothetical prote
90	29	25.9	30	1	A23483	alcohol oxidase (B
91	29	25.9	33	2	S13863	dihydroliipoamide d
92	29	25.9	41	2	S00266	dipteracin B - nes
93	29	25.9	43	2	D58213	protamine III - Am
94	29	25.9	43	2	S41388	protein 3a - human
95	29	25.9	44	2	D82579	hypothetical prote
96	29	25.9	45	2	B35156	dihydroliipoamide d
97	28	25.0	10	2	D60787	sperm-activating p
98	28	25.0	10	2	D60527	sperm-activating p
99	28	25.0	12	2	S70337	napin small chain
100	28	25.0	18	2	S09722	2S albumin small c

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:08:33 ; Search time 131.111 Seconds
(without alignments)
58.997 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGGGGGGGGGGGGGGGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1980s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	20	2	AAR87737
2	112	100.0	20	2	AAW18554
3	112	100.0	20	2	AAW18554
4	112	100.0	20	3	AAW18554
5	112	100.0	20	5	ABP51824
6	112	100.0	20	5	ABG78248
7	112	100.0	20	5	AAU75147
8	112	100.0	20	5	AAE21140
9	112	100.0	20	5	ABG91939
10	112	100.0	20	6	ABR57056
11	112	100.0	20	6	AAE37194
12	112	100.0	20	6	ABP60059
13	112	100.0	20	6	AAW79954
14	112	100.0	20	6	ABR62592
15	112	100.0	20	7	AAE38680
16	112	100.0	20	7	ADG34709
17	112	100.0	20	7	ADP44885
18	112	100.0	20	7	ADN97318
19	112	100.0	20	7	ADN97316
20	112	100.0	20	8	ADG42781
21	112	100.0	20	8	ADI04108
22	112	100.0	20	8	ADM8280
23	112	100.0	20	8	ADO21851
24	112	100.0	20	8	ADN91462
25	112	100.0	20	8	ADT62591

26	112	100.0	21	8	ADR49619	Human Igg
27	112	100.0	22	2	AAR87736	Spacer #4
28	112	100.0	24	2	AAW23689	Stalling
29	112	100.0	24	3	AAW94379	Zinc fing
30	112	100.0	24	8	ADM95078	Poly-glyc
31	112	100.0	25	2	AAW18555	Linker se
32	112	100.0	25	2	AAW10303	Peptide 1
33	112	100.0	25	6	AAW39013	Synthetic
34	112	100.0	25	7	ABU64228	HIV gp 16
35	112	100.0	25	8	ADM95077	Poly-glyc
36	112	100.0	25	8	ADO21852	Histone a
37	112	100.0	25	8	ADQ77071	Peptide 1
38	112	100.0	26	8	ADL24301	Cardiovas
39	112	100.0	28	2	AAW25360	IFNAR2/IF
40	112	100.0	30	4	AAW77868	MHC class
41	112	100.0	30	6	AAE37195	Linker pe
42	112	100.0	30	6	ADN00801	Epitope p
43	112	100.0	30	8	ADO21853	Histone a
44	112	100.0	30	8	ADP48740	Linker pe
45	112	100.0	32	3	AAW00160	Linker pe
46	112	100.0	33	2	AAW25359	IFNAR2/IF
47	112	100.0	35	3	AAW00157	Seven rep
48	112	100.0	35	6	ABJ39015	Synthetic
49	112	100.0	35	8	ADQ77072	Peptide 1
50	112	100.0	39	3	AAW00159	Seven rep
51	112	100.0	40	3	AAW87573	Linker be
52	112	100.0	40	6	ABU09677	INF-beta-
53	112	100.0	40	6	AAE37196	Linker pe
54	112	100.0	40	8	ADQ28273	Peptide 1
55	108	96.4	20	5	AAO17003	Linker pe
56	108	96.4	20	6	ADB24914	Peptide 1
57	108	96.4	20	7	ADB24914	Peptide 1
58	108	96.4	20	7	ABU10016	Alpha-MSH
59	108	96.4	20	8	ADQ28275	Peptide 1
60	108	96.4	41	6	ABR56404	Peptide 1
61	108	96.4	41	6	ABR44505	Peptide 1
62	106	94.6	23	6	ABU09675	INF-beta-
63	106	94.6	33	6	ABR56402	Peptide 1
64	106	94.6	33	6	ABR44503	Peptide 1
65	102	91.1	30	6	ABU09676	INF-beta-
66	100	89.3	22	7	ABU64227	HIV gp 16
67	98	87.5	22	8	ADG47235	TNF-R lin
68	96	85.7	18	6	ABJ39014	Synthetic
69	96	85.7	20	4	AAW69491	Synthetic
70	96	85.7	20	5	AAE28377	Peptide #
71	96	85.7	20	7	ADH44251	Spacer am
72	96	85.7	20	8	ADF12141	Transfect
73	96	85.7	21	4	AAW69492	Synthetic
74	96	85.7	23	2	AAW67767	Platelet
75	96	85.7	24	2	AAW79139	GG24 Gly
76	96	85.7	29	8	ADQ80634	Binding d
77	96	85.7	33	5	AAE28394	NLS based
78	96	85.7	33	8	ADH44268	Transfect
79	96	85.7	33	8	ADF12158	Exemplary
80	96	85.7	37	7	ADI19998	Linker-my
81	96	85.7	38	7	ADH22061	Synthetic
82	96	85.7	50	2	AAW13632	Apollipop
83	96	85.7	50	2	AAW13633	Apollipop
84	94	83.9	38	8	ADG74171	Linker pe
85	92	82.1	29	4	AAW58600	Peptide e
86	91	81.2	21	8	ADQ80631	Binding d
87	90	80.4	16	8	ADR49618	Linker pe
88	90	80.4	17	5	AAE22931	Linker pe
89	90	80.4	17	5	AAE23006	Linker pe
90	90	80.4	18	3	AAW43500	Linker fo
91	90	80.4	18	3	AAW83214	Peptide 1
92	90	80.4	18	5	AAE22938	Linker pe
93	90	80.4	18	6	ABU09674	INF-beta-
94	90	80.4	30	6	AAE32929	Fc fusion
95	90	80.4	30	6	AAE32930	Fc fusion
96	90	80.4	30	6	AAE32642	Fc fusion
97	90	80.4	30	6	AAE32641	Fc fusion
98	90	80.4	30	7	ADF75015	Human Igg

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:22:24 ; Search time 93.3333 Seconds
(without alignments)
65.078 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGGGGGGGGGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 525249

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Databases :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	9	US-09-767-395-31
2	84	100.0	15	9	US-09-287-849-46
3	84	100.0	15	9	US-09-147-142-29
4	84	100.0	15	9	US-09-782-650-8
5	84	100.0	15	9	US-09-766-543-6
6	84	100.0	15	9	US-09-746-359A-72
7	84	100.0	15	9	US-09-808-037-2
8	84	100.0	15	9	US-09-976-787-17
9	84	100.0	15	9	US-09-911-610-5
10	84	100.0	15	9	US-09-865-198-17
11	84	100.0	15	9	US-09-759-352-45
12	84	100.0	15	9	US-09-767-395-31
13	84	100.0	15	9	US-09-287-849-46
14	84	100.0	15	9	US-09-147-142-29
15	84	100.0	15	9	US-09-782-650-8
16	84	100.0	15	9	US-09-766-543-6
17	84	100.0	15	9	US-09-746-359A-72
18	84	100.0	15	9	US-09-808-037-2
19	84	100.0	15	9	US-09-976-787-17
20	84	100.0	15	9	US-09-911-610-5
21	84	100.0	15	9	US-09-865-198-17
22	84	100.0	15	9	US-09-759-352-45

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:14:03 ; Search time 89 Seconds

(without alignments)

86.305 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGGGGGGGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	85.7	15	2 Q9S8K3	Q9S8K3 glycine max
2	70	83.3	25	2 Q42086	Q42086 arabidopsis
3	66	78.6	45	2 Q7R2M4	Q7R2M4 neurospora
4	62	73.8	28	2 Q37931	Q37931 bacterioph
5	62	73.8	36	2 Q02023	Q02023 lycopersico
6	62	73.8	43	1 GRW1_LYCES	Q01157 lycopersico
7	62	73.8	49	2 P93517	P93517 zea mays (m
8	59	70.2	42	2 Q23471	Q23471 arabidopsis
9	58	69.0	47	2 Q9S857	Q9S857 glycine max
10	55	65.5	50	2 Q943L9	Q943L9 oryza sativ
11	54	64.3	26	2 Q42226	Q42226 arabidopsis
12	54	64.3	43	2 Q8QUM1	Q8QUM1 infectious
13	53	63.1	50	2 Q8N008	Q8N008 plasmodium
14	53	63.1	50	2 Q8N009	Q8N009 plasmodium
15	51	60.7	34	2 Q7M322	Q7M322 fasciola he
16	51	60.7	46	2 Q708X1	Q708X1 cicier ariet
17	50	59.5	45	1 YD27_HABIN	F44163 haemophilus
18	50	59.5	47	2 Q81U37	Q81U37 bacillus an
19	49.5	58.9	20	2 Q9UR60	Q9UR60 candida alb
20	49	58.3	50	2 Q7X187	Q7X187 oryza sativ
21	48	57.1	36	2 Q6X920	Q6X920 equus cabal
22	48	57.1	47	2 Q73CB1	Q73CB1 bacillus ce
23	48	57.1	50	2 Q6K325	Q6K325 oryza sativ
24	48	57.1	50	2 Q73CM9	Q73CM9 bacillus ce
25	47	56.0	27	1 FBRL_PHYPO	P22508 physarum po
26	47	56.0	43	2 Q63281	Q63281 rattus norv
27	47	56.0	50	1 YK05_CABEL	P34300 caenorhabdi
28	46	54.8	20	2 Q81ZT3	Q81ZT3 homo sapien
29	46	54.8	35	2 Q64L91	Q64L91 gulo gulo (
30	46	54.8	41	2 Q99PH5	Q99PH5 mus musculu
31	46	54.8	45	2 Q7XMY7	Q7XMY7 oryza sativ

32	45.5	54.2	41	2	Q9TMZ5	Q9TMZ5 rattus norv
33	45.5	54.2	44	2	Q9S562	Q9S562 rattus norv
34	45	53.6	46	2	Q81RP8	Q81RP8 bacillus an
35	45	53.6	48	2	Q60413	Q60413 cricetus cr
36	45	53.6	50	2	Q81UD0	Q81UD0 bacillus an
37	44.5	53.0	46	2	Q6A186	Q6A186 cryptospori
38	44	52.4	35	2	Q6LC06	Q6LC06 homo sapien
39	44	52.4	32	2	Q94214	Q94214 oryza sativ
40	44	52.4	40	2	Q9BDE8	Q9BDE8 sus scrofa
41	44	52.4	40	2	Q8ERB7	Q8ERB7 oceanobacil
42	44	52.4	43	2	Q65L83	Q65L83 bacillus li
43	43.5	51.8	31	1	FBRL_RAT	P22509 rattus norv
44	43	51.2	34	2	Q6VV38	Q6VV38 human herpe
45	43	51.2	40	2	Q6MMI6	Q6MMI6 bdellovibri
46	43	51.2	41	2	Q9TVQ8	Q9TVQ8 pseudotetia
47	43	51.2	47	2	Q8N010	Q8N010 plasmodium
48	42.5	50.6	34	2	Q8JOA0	Q8JOA0 athroderma
49	42.5	50.6	34	2	Q8JL17	Q8JL17 trichophyto
50	42	50.0	44	2	Q9Y199	Q9Y199 cyprinus ca
51	42	50.0	49	2	Q9SCS1	Q9SCS1 arabidopsis
52	41.5	49.4	21	2	Q9R204	Q9R204 mus musculu
53	41.5	49.4	49	2	Q62SA3	Q62SA3 bacillus li
54	41.5	49.4	50	2	Q8XY14	Q8XY14 talstonia s
55	41	48.8	16	2	Q7JNE8	Q7JNE8 drosophila
56	41	48.8	17	1	H4_SEPOF	Q7M3Z5 sepia offic
57	41	48.8	20	2	Q7M3Z6	Q7M3Z6 hemicecentrot
58	41	48.8	20	2	Q8W238	Q8W238 glycine max
59	41	48.8	23	2	P70093	P70093 xenopus lae
60	41	48.8	24	1	H4_NEDSA	Pe2789 medicago sa
61	41	48.8	33	2	Q17071	Q17071 antheraea p
62	41	48.8	33	2	Q27637	Q27637 drosophila
63	41	48.8	34	2	Q27821	Q27821 trichomonas
64	41	48.8	34	2	Q6VV39	Q6VV39 human herpe
65	41	48.8	35	2	Q27754	Q27754 pisaster oc
66	41	48.8	49	1	YK06_CABEL	F34301 caenorhabdi
67	41	48.8	50	1	YK02_CABEL	F34297 caenorhabdi
68	40	47.6	22	2	Q17072	Q17072 antheraea p
69	40	47.6	27	2	Q9XJ05	Q9XJ05 oryza sativ
70	40	47.6	34	2	Q9A4N0	Q9A4N0 caulobacter
71	40	47.6	34	2	Q6VV29	Q6VV29 human herpe
72	40	47.6	35	2	Q6F345	Q6F345 oryza sativ
73	40	47.6	42	2	Q8MXU9	Q8MXU9 caenorhabdi
74	40	47.6	44	2	Q6Y1D5	Q6Y1D5 lactuca sat
75	39	46.4	20	2	Q7JMY8	Q7JMY8 leishmania
76	39	46.4	23	2	Q9UC00	Q9UC00 homo sapien
77	39	46.4	34	2	Q9TVM6	Q9TVM6 ichtyophth
78	39	46.4	48	2	Q8YUR2	Q8YUR2 anabaena sp
79	38	45.2	22	2	Q6V0X7	Q6V0X7 serratia ma
80	38	45.2	40	2	Q65SK6	Q65SK6 manheimia
81	38	45.2	47	1	H4Y_BLEJA	P80738 blepharisma
82	38	45.2	48	2	Q6JDL2	Q6JDL2 canis famil
83	38	45.2	50	2	Q9N120	Q9N120 plasmodium
84	37	44.0	44	2	Q8N011	Q8N011 plasmodium
85	37	44.0	44	2	Q8N011	Q8N011 plasmodium
86	37	44.0	46	2	Q55688	Q55688 hepatitis e
87	36.5	43.5	42	2	Q9PWJ2	Q9PWJ2 cyprinus ca
88	36	42.9	11	2	Q75ML1	Q75ML1 homo sapien
89	36	42.9	23	2	Q9UP87	Q9UP87 homo sapien
90	36	42.9	23	2	Q9TWK2	Q9TWK2 mytilus edu
91	36	42.9	35	2	Q73CM5	Q73CM5 bacillus ce
92	36	42.9	40	2	Q8S5P4	Q8S5P4 oryza sativ
93	36	42.9	47	2	Q9XXD3	Q9XXD3 caenorhabdi
94	35.5	42.3	50	2	Q84Y85	Q84Y85 oryza sativ
95	35	41.7	10	2	Q7M3T9	Q7M3T9 tripeustes
96	35	41.7	17	2	Q9RAY9	Q9RAY9 alcaligenes
97	35	41.7	23	2	Q7M3Q9	Q7M3Q9 fasciola he
98	35	41.7	31	2	Q03891	Q03891 tetrahymena
99	35	41.7	31	2	Q03892	Q03892 tetrahymena
100	35	41.7	31	2	Q03893	Q03893 tetrahymena

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:15:03 ; Search time 19 Seconds
(without alignments)
75.961 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GCGSGGGGCGGGS 15

Scoring table: BLOSUM62

Scoring rule: $\text{Gapop} \cdot 10 + \text{Gapext}$

Searched: 283416 seqs. 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq	length: 50
Maximum DB seq	length: 50

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 100 summaries

Database : PTR 79.*

```
Database :
          PLK_79:*
          1:  pirl:*
```

```
1: pir1: *
2: pir2: *
```

```

2:  pir2: *
3:  pir3: *

```

```
3: pi13: *
4: pi14: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
1	62	73.8	49	2	T02026	glycine-rich prote	
2	59	70.2	42	2	A71429	hypothetical prote	
3	52	61.9	12	2	A58375	microcin B17 - Esc	
4	51	60.7	34	2	A61184	preselenitized egg	
5	50	59.5	45	2	A64026	hypothetical prote	
6	47	56.0	27	2	A31508	34K nucleolar prot	
7	47	56.0	50	2	C88533	hypothetical prote	
8	43.5	51.8	31	2	A23887	fibrillarin - rat	
9	43	51.2	29	2	S06854	chorion class B pr	
10	42	50.0	49	2	A74085	hypothetical prote	
11	41	48.8	17	2	B61321	histone H4 - chick	
12	41	48.8	17	2	A61321	histone H4 - commo	
13	41	48.8	20	2	S68620	histone H4 - sea u	
14	41	48.8	23	2	I51431	histone H4-1 precu	
15	41	48.8	24	2	B43295	histone H4 - alfal	
16	41	48.8	35	2	A28663	histone H4 - starf	
17	41	48.8	39	2	D88533	5.0K hypothetical	
18	40	47.6	34	2	H87595	hypothetical prote	
19	39	46.4	48	2	AB2090	hypothetical prote	
20	36	42.9	47	2	T28981	hypothetical prote	
21	35	41.7	10	2	F60527	sperm-activating p	
22	35	41.7	23	2	A32473	histidine-rich pro	
23	35	41.7	31	2	S10260	histone H4.2 - Tet	
24	35	41.7	31	2	S10262	histone H4.2 - Tet	
25	35	41.7	31	2	S10264	histone H4.2 - Tet	
26	35	41.7	31	2	S10268	histone H4.2 - Tet	
27	35	41.7	31	2	S10266	histone H4.2 - Tet	
28	35	41.7	31	2	S10270	histone H4.2 - Tet	
29	35	41.7	31	2	S10272	histone H4.2 - Tet	

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:08:33 ; Search time 98.3333 Seconds
(without alignments)
58.997 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGGGGGGGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	2	AAR25983 Peptide m
2	84	100.0	15	2	AAR59500 Hydrophil
3	84	100.0	15	2	AAR85123 Gene deli
4	84	100.0	15	2	AAR76683 Human ONS
5	84	100.0	15	2	AAR99244 (Gly4ser)
6	84	100.0	15	2	AAR95067 scFv spac
7	84	100.0	15	2	AAR93223 Peptide 1
8	84	100.0	15	2	AAY49219 Sequence
9	84	100.0	15	2	AAW10295 Peptide 1
10	84	100.0	15	2	AAW35984 Peptide 1
11	84	100.0	15	2	AAW87784 Antibody-
12	84	100.0	15	2	AAY43414 Peptide S
13	84	100.0	15	2	AAY33328 E6-sfv pe
14	84	100.0	15	2	AAY03763 Linker pe
15	84	100.0	15	2	AAY21600 EP-919566
16	84	100.0	15	2	AAY27397 Flexible
17	84	100.0	15	2	AAR16564 Peptide 1
18	84	100.0	15	3	AAB29542 Linker pe
19	84	100.0	15	3	AAY99636 (Gly4ser)
20	84	100.0	15	3	AAB22838 Single ch
21	84	100.0	15	3	AAY70606 Protein e
22	84	100.0	15	3	AAY79551 Linker pe
23	84	100.0	15	3	AAY79552 Linker pe
24	84	100.0	15	3	AAY90826 Linker am
25	84	100.0	15	3	AAB23816 Plasmid p

26	84	100.0	15	3	AA97237	Aay97237 Peptide 1
27	84	100.0	15	3	AAAB15682	Aab15682 Single-ch
28	84	100.0	15	4	AAAB70169	Aab70169 Gly/ser l
29	84	100.0	15	4	AAAB98920	Aab98920 Linker pe
30	84	100.0	15	4	AAAE13082	Aae13082 Glycine l
31	84	100.0	15	4	AAAM52571	Aam52571 Peptide 1
32	84	100.0	15	4	AAAE12408	Aae12408 Peptide 1
33	84	100.0	15	4	AAAU08689	Aau08689 Antibody
34	84	100.0	15	4	AAAE06268	Aae06268 Glycine l
35	84	100.0	15	4	AAAU09970	Aau09970 Glycine-S
36	84	100.0	15	4	AAAU04948	Aau04948 Humanised
37	84	100.0	15	4	AAAE13100	Aae13100 Linker pe
38	84	100.0	15	4	AAAB79010	Aab79010 Peptide 1
39	84	100.0	15	4	AAAB97229	Aab97229 Immunoglo
40	84	100.0	15	4	AAAB85296	Aab85296 Sequence
41	84	100.0	15	4	AAAU29009	Aau29009 Tumour-sp
42	84	100.0	15	4	AAAB58601	Aab58601 Peptide e
43	84	100.0	15	4	AAAB48032	Aab48032 Gly-Ser p
44	84	100.0	15	4	AAAB61572	Aab61572 Flexible
45	84	100.0	15	4	AAAB74579	Aab74579 Context-d
46	84	100.0	15	5	ABG67227	Abg67227 Interleuk
47	84	100.0	15	5	ABP51823	Abp51823 Fusion pr
48	84	100.0	15	5	AAAU86039	Aau86039 Human glu
49	84	100.0	15	5	AAAU82112	Aau82112 T-cell sp
50	84	100.0	15	5	AAAE28918	Aae28918 Peptide 1
51	84	100.0	15	5	AAAU11449	Aau11449 Synthetic
52	84	100.0	15	5	AAE23425	Aae23425 Linker pe
53	84	100.0	15	5	ABBS98375	Abbs98375 Human VEG
54	84	100.0	15	5	AAAE18134	Aae18134 Peptide u
55	84	100.0	15	5	ABBB84084	Abb84084 Human scd
56	84	100.0	15	5	ABG78249	Abg78249 Human Fv
57	84	100.0	15	5	AAAM47630	Aam47630 Linker se
58	84	100.0	15	5	ABP53557	Abp53557 Peptide 1
59	84	100.0	15	5	ABG63325	Abg63325 Synthetic
60	84	100.0	15	5	ABBY9500	Abby9500 Peptide 1
61	84	100.0	15	5	AAU99371	Aau99371 Peptide 1
62	84	100.0	15	5	AAE25957	Aae25957 Linker pe
63	84	100.0	15	5	ABG97825	Abg97825 Gly-Ser l
64	84	100.0	15	5	ABG97807	Abg97807 Synthetic
65	84	100.0	15	5	ABG68874	Abg68874 GGGGS lin
66	84	100.0	15	5	ABG73658	Abg73658 hdm2-asfo
67	84	100.0	15	5	ABG35328	Abg35328 Thrombopo
68	84	100.0	15	5	ABG35310	Abg35310 Thrombopo
69	84	100.0	15	5	AAE29080	Aae29080 Linker pe
70	84	100.0	15	5	AAE22203	Aae22203 Peptide 1
71	84	100.0	15	5	AAU75757	Aau75757 Peptide 1
72	84	100.0	15	5	ABG77165	Abg77165 Flexible
73	84	100.0	15	5	ABG31061	Abg31061 Angiogene
74	84	100.0	15	5	AAU76997	Aau76997 Immunoglo
75	84	100.0	15	5	AAU80037	Aau80037 Spacer pe
76	84	100.0	15	5	AAO22077	Aao22077 15 amino
77	84	100.0	15	5	ABG91940	Abg91940 Human ant
78	84	100.0	15	5	ABG32859	Abg32859 Linker pe
79	84	100.0	15	5	AAU75385	Aau75385 Immunotox
80	84	100.0	15	5	AAU75398	Aau75398 Immunotox
81	84	100.0	15	5	ABG32899	Abg32899 Peptide 1
82	84	100.0	15	6	ABU11014	Abu11014 Synthetic
83	84	100.0	15	6	AAO26602	Aao26602 Fusion pr
84	84	100.0	15	6	AAO16063	Aao16063 Neurologi
85	84	100.0	15	6	ABP56234	Abp56234 Single ch
86	84	100.0	15	6	AAE36052	Aae36052 Single ch
87	84	100.0	15	6	ABU08978	Abu08978 (G4S) 3 ep
88	84	100.0	15	6	ABJ26809	Abj26809 VEGF bind
89	84	100.0	15	6	ABJ26726	Abj26726 VEGF bind
90	84	100.0	15	6	ABR42598	Abra42598 Peptide 1
91	84	100.0	15	6	AAE37114	Aae37114 Linker pe
92	84	100.0	15	6	ABJ19272	Abj19272 Anti-huma
93	84	100.0	15	6	ABR55699	Abbr55699 Linker pe
94	84	100.0	15	6	ABP97415	Abp97415 E4B7-deri
95	84	100.0	15	6	AAE30958	Aae30958 Linker pe
96	84	100.0	15	6	AAE30956	Aae30956 Linker pe
97	84	100.0	15	6	ABG72723	Abg72723 Linker pe
98	84	100.0	15	6	ABO23257	Abob23257 Light cha

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:22:24 ; Search time 62.2222 Seconds
(without alignments)
65.078 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGGGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 525249

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	9	US-09-789-922-5
2	56	100.0	10	9	US-09-287-849-45
3	56	100.0	10	9	US-09-147-142-30
4	56	100.0	10	9	US-09-376-787-19
5	56	100.0	10	9	US-09-865-198-19
6	56	100.0	10	9	US-09-790-317-6
7	56	100.0	10	10	US-09-798-689-19
8	56	100.0	10	10	US-09-984-010-16
9	56	100.0	10	10	US-09-949-039-36
10	56	100.0	10	10	US-09-833-203-7
11	56	100.0	10	13	US-10-115-984-7
					Sequence 5, Appli
					Sequence 45, Appl
					Sequence 30, Appl
					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 6, Appli
					Sequence 16, Appl
					Sequence 19, Appl
					Sequence 36, Appl
					Sequence 7, Appli

12	56	100.0	10	14	US-10-082-671-7	Sequence 7, Appli
13	56	100.0	10	14	US-10-282-121-4	Sequence 4, Appli
14	56	100.0	10	14	US-10-252-408-29	Sequence 29, Appl
15	56	100.0	10	14	US-10-021-818-5	Sequence 5, Appli
16	56	100.0	10	14	US-10-288-250-8	Sequence 8, Appli
17	56	100.0	10	14	US-10-262-828A-5	Sequence 5, Appli
18	56	100.0	10	14	US-10-359-460-45	Sequence 45, Appl
19	56	100.0	10	15	US-10-359-459-9	Sequence 9, Appli
20	56	100.0	10	15	US-10-296-317-96	Sequence 96, Appl
21	56	100.0	10	15	US-10-622-108-28	Sequence 28, Appl
22	56	100.0	10	15	US-10-367-956-30	Sequence 30, Appl
23	56	100.0	10	15	US-10-645-000-18	Sequence 18, Appl
24	56	100.0	10	16	US-10-666-871-17	Sequence 17, Appl
25	56	100.0	10	16	US-10-666-886-17	Sequence 17, Appl
26	56	100.0	10	16	US-10-646-308-34	Sequence 34, Appl
27	56	100.0	10	16	US-10-724-178-19	Sequence 19, Appl
28	56	100.0	10	16	US-10-666-898-17	Sequence 17, Appl
29	56	100.0	10	16	US-10-666-834-17	Sequence 17, Appl
30	56	100.0	10	16	US-10-772-021-1	Sequence 1, Appli
31	56	100.0	10	16	US-10-667-193-17	Sequence 17, Appl
32	56	100.0	10	16	US-10-667-166-17	Sequence 17, Appl
33	56	100.0	10	16	US-10-666-833-17	Sequence 17, Appl
34	56	100.0	10	16	US-10-482-630-19	Sequence 19, Appl
35	56	100.0	10	16	US-10-778-910-19	Sequence 19, Appl
36	56	100.0	10	16	US-10-634-740-8	Sequence 8, Appli
37	56	100.0	10	17	US-10-885-225-147	Sequence 147, App
38	56	100.0	10	17	US-10-495-491-10	Sequence 10, Appl
39	56	100.0	10	17	US-10-668-073-17	Sequence 17, Appl
40	56	100.0	10	17	US-10-792-498-30	Sequence 30, Appl
41	56	100.0	10	17	US-10-954-094-147	Sequence 147, App
42	56	100.0	11	13	US-10-115-817-5	Sequence 5, Appli
43	56	100.0	11	14	US-10-247-954-5	Sequence 5, Appli
44	56	100.0	11	14	US-10-081-281-38	Sequence 38, Appl
45	56	100.0	12	14	US-10-005-438-5	Sequence 5, Appli
46	56	100.0	12	15	US-10-296-317-29	Sequence 29, Appl
47	56	100.0	12	17	US-10-917-899-5	Sequence 5, Appli
48	56	100.0	13	17	US-10-485-545A-2	Sequence 2, Appli
49	56	100.0	13	9	US-09-359-672-4	Sequence 4, Appli
50	56	100.0	13	16	US-10-806-422-60	Sequence 60, Appl
51	56	100.0	13	17	US-10-485-545A-15	Sequence 15, Appl
52	56	100.0	14	9	US-09-815-837-108	Sequence 108, App
53	56	100.0	14	9	US-09-766-378A-29	Sequence 29, Appl
54	56	100.0	14	9	US-09-850-715-16	Sequence 16, Appl
55	56	100.0	14	14	US-10-232-838-20	Sequence 20, Appl
56	56	100.0	14	15	US-10-247-839-89	Sequence 89, Appl
57	56	100.0	14	15	US-10-247-839-101	Sequence 101, App
58	56	100.0	14	15	US-10-621-693-61	Sequence 61, Appl
59	56	100.0	14	16	US-10-742-161-5	Sequence 5, Appli
60	56	100.0	14	16	US-10-742-372-5	Sequence 5, Appli
61	56	100.0	15	9	US-09-767-395-31	Sequence 31, Appl
62	56	100.0	15	9	US-09-287-849-46	Sequence 46, Appl
63	56	100.0	15	9	US-09-147-142-29	Sequence 29, Appl
64	56	100.0	15	9	US-09-782-650-8	Sequence 8, Appli
65	56	100.0	15	9	US-09-766-543-6	Sequence 6, Appli
66	56	100.0	15	9	US-09-746-359A-72	Sequence 72, Appl
67	56	100.0	15	9	US-09-808-037-2	Sequence 2, Appli
68	56	100.0	15	9	US-09-911-610-5	Sequence 5, Appli
69	56	100.0	15	9	US-09-865-198-17	Sequence 17, Appl
70	56	100.0	15	9	US-09-759-352-45	Sequence 45, Appl
71	56	100.0	15	9	US-09-867-262-4	Sequence 4, Appli
72	56	100.0	15	9	US-09-747-689-7	Sequence 7, Appli
73	56	100.0	15	9	US-09-987-456-6	Sequence 6, Appli
74	56	100.0	15	9	US-09-987-456-7	Sequence 7, Appli
75	56	100.0	15	9	US-09-753-126-23	Sequence 23, Appl
76	56	100.0	15	9	US-09-885-551A-4	Sequence 4, Appli
77	56	100.0	15	9	US-09-990-205-5	Sequence 5, Appli
78	56	100.0	15	9	US-09-144-886-1	Sequence 1, Appli
79	56	100.0	15	9	US-09-956-206A-67	Sequence 67, Appl
80	56	100.0	15	9	US-09-968-561A-6	Sequence 6, Appli
81	56	100.0	15	9	US-09-887-853-7	Sequence 7, Appli
82	56	100.0	15	10	US-09-939-769-96	Sequence 96, Appl
83	56	100.0	15	10	US-09-749-873-111	Sequence 111, App

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:14:03 ; Search time 59.3333 Seconds
(without alignments)
86.305 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGSGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	85.7	15	2 Q98K3	Q98K3 glycine max
2	48	85.7	25	2 Q42086	Q42086 arabidopsis
3	48	85.7	45	2 Q75ZM4	Q75ZM4 neurospora
4	47	83.9	36	2 Q02023	Q02023 lycopersico
5	47	83.9	43	1 GRW1_LYCES	GRW1_LYCES
6	46	82.1	45	2 Q7XMY7	Q7XMY7 oryza sativ
7	46	82.1	49	2 P93517	P93517 zea mays
8	44	78.6	28	2 Q37931	Q37931 bacterioph
9	43	76.8	42	2 Q23471	Q23471 arabidopsis
10	43	76.8	47	2 Q98857	Q98857 glycine max
11	42	75.0	20	2 Q81Z13	Q81Z13 homo sapien
12	41	73.2	43	2 Q63281	Q63281 rattus norv
13	41	73.2	45	1 YD27_HAEIN	YD27_HAEIN
14	41	73.2	47	2 Q8N010	Q8N010 plasmodium
15	41	73.2	50	2 Q8N008	Q8N008 plasmodium
16	41	73.2	50	2 Q8N009	Q8N009 plasmodium
17	41	73.2	50	2 Q943L9	Q943L9 oryza sativ
18	41	73.2	50	2 Q7X187	Q7X187 oryza sativ
19	40	71.4	41	2 Q99PH5	Q99PH5 mus musculu
20	40	71.4	44	2 Q6V1D5	Q6V1D5 lactuca sat
21	38	67.9	40	2 Q6MMI6	Q6MMI6 bdellovibri
22	38	67.9	46	2 Q81RP8	Q81RP8 bacillus an
23	38	67.9	47	2 Q73CB1	Q73CB1 bacillus an
24	37	66.1	47	2 Q73CB1	Q73CB1 bacillus ce
25	37	66.1	49	2 Q9SCS1	Q9SCS1 arabidopsis
26	37	66.1	50	2 Q6K325	Q6K325 oryza sativ
27	36	64.3	11	2 Q75ML1	Q75ML1 homo sapien
28	36	64.3	20	2 Q9UR60	Q9UR60 candida alb
29	36	64.3	26	2 Q42226	Q42226 arabidopsis
30	36	64.3	27	2 Q9XJ05	Q9XJ05 oryza sativ
31	36	64.3	34	2 Q7M3Z2	Q7M3Z2 fasciola he

32	64.3	36	2	Q6X9Z0	Q6X9Z0 equus cabal
33	64.3	36	2	Q8QUM1	Q8QUM1 infectious
34	62.5	35	20	Q8W238	Q8W238 glycine max
35	62.5	35	40	Q9BDE8	Q9BDE8 sus scrofa
36	62.5	35	44	2 Q8N011	Q8N011 plasmodium
37	62.5	35	46	2 Q6A186	Q6A186 cryptospori
38	62.5	35	46	2 Q708X1	Q708X1 cicor ariet
39	60.7	34	2	Q6X2S9	Q6X2S9 homo sapien
40	60.7	34	10	2 Q6X2S9	Q6X2S9 homo sapien
41	60.7	34	15	2 Q9TWE1	Q9TWE1 plasmodium
42	60.7	34	17	1 PFK5_PERAM	PFK5_PERAM
43	60.7	34	17	2 Q9R4Y9	Q9R4Y9 periplaneta
44	60.7	34	20	2 Q9UP87	Q9UP87 alcaligenes
45	60.7	34	27	2 Q9UNT8	Q9UNT8 homo sapien
46	60.7	34	31	2 O5S182	O5S182 rattus norv
47	60.7	34	31	2 Q7QYA2	Q7QYA2 giardia lam
48	60.7	34	34	2 Q6VV38	Q6VV38 human herpe
49	60.7	35	35	2 Q64L91	Q64L91 gulo gulo
50	60.7	34	39	2 Q16457	Q16457 homo sapien
51	60.7	34	40	2 Q8WT12	Q8WT12 plasmodium
52	60.7	34	40	2 Q9L8R9	Q9L8R9 staphylococ
53	60.7	34	40	2 Q9X968	Q9X968 salmonella
54	60.7	34	43	2 Q7GLJ2	Q7GLJ2 zea mays
55	60.7	34	43	2 Q6SL83	Q6SL83 bacillus li
56	60.7	34	44	2 Q8F413	Q8F413 leptospira
57	60.7	34	44	2 Q9YI99	Q9YI99 cyprinus ca
58	60.7	34	46	2 Q9K2J4	Q9K2J4 staphylococ
59	60.7	34	46	2 O5S688	O5S688 hepatitis e
60	60.7	34	48	2 Q6JDL2	Q6JDL2 canis fami
61	60.7	34	50	2 Q73CM9	Q73CM9 bacillus ce
62	60.7	34	50	2 Q677X2	Q677X2 lymphocysti
63	58.9	33	27	1 Q7JMY8	Q7JMY8 leishmania
64	58.9	33	27	2 Q6VV44	Q6VV44 human herpe
65	58.9	33	34	2 Q9TVQ8	Q9TVQ8 pseudotetia
66	58.9	33	42	2 Q8MXU9	Q8MXU9 caenorhabdi
67	58.0	32	42	2 Q9PWJ2	Q9PWJ2 cyprinus ca
68	57.1	32	21	2 Q9R5U9	Q9R5U9 rhodococcus
69	57.1	32	21	2 Q9R204	Q9R204 mus musculu
70	57.1	32	31	1 F8RL_RAT	F8RL_RAT
71	57.1	32	31	1 Q9TVM6	Q9TVM6 ichthyophth
72	57.1	34	34	2 Q6VV29	Q6VV29 human herpe
73	57.1	34	34	2 Q6VV39	Q6VV39 human herpe
74	57.1	35	35	2 Q942I4	Q942I4 oryza sativ
75	57.1	40	40	2 Q8S5P4	Q8S5P4 oryza sativ
76	57.1	41	41	2 Q75IG2	Q75IG2 oryza sativ
77	57.1	48	48	2 Q60413	Q60413 cricetus cr
78	57.1	48	48	2 Q60413	Q60413 cricetus cr
79	57.1	50	50	2 Q84YS5	Q84YS5 oryza sativ
80	57.1	50	50	2 Q81UD0	Q81UD0 bacillus an
81	56.2	50	50	2 Q9R5P8	Q9R5P8 nocardiopsi
82	55.4	10	2	Q7M3T9	Q7M3T9 tripneustes
83	55.4	16	2	Q7JNE8	Q7JNE8 drosophila
84	55.4	17	1	H4_SEPOF	H4_SEPOF
85	55.4	20	2	Q7M3Z5	Q7M3Z5 sepi offic
86	55.4	23	2	P70093	P70093 xenopus lae
87	55.4	24	1	H4_MEDSA	H4_MEDSA
88	55.4	32	1	YL55_CAEBL	YL55_CAEBL
89	55.4	33	2	Q27637	Q27637 drosophila
90	55.4	34	2	Q27821	Q27821 trichomonas
91	55.4	34	2	Q9A4N0	Q9A4N0 caulobacter
92	55.4	35	2	Q27754	Q27754 piaster oc
93	55.4	35	2	Q6F345	Q6F345 oryza sativ
94	55.4	39	2	Q64160	Q64160 bacterioph
95	55.4	39	2	O31888	O31888 bacillus su
96	55.4	40	2	Q8ERB7	Q8ERB7 oceanobacil
97	55.4	41	2	Q9TNZ5	Q9TNZ5 rattus norv
98	55.4	44	2	Q9S562	Q9S562 rattus norv
99	55.4	46	2	Q75MQ8	Q75MQ8 homo sapien
100	55.4	46	2	Q6T345	Q6T345 quercus rob

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:15:03 ; Search time 12.6667 Seconds
(without alignments)
75.961 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGSGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	85.7	12	A58375	microcin B17 - Esc
2	46	82.1	49	T02026	glycine-rich prote
3	43	76.8	42	A71429	hypothetical prote
4	41	73.2	45	A64026	hypothetical prote
5	37	66.1	49	T46085	hypothetical prote
6	36	64.3	34	A61184	presclerotized egg
7	34	60.7	15	S62609	glutathione-disulf
8	33	58.9	27	A31508	34K nucleolar prot
9	32	57.1	28	P00263	dnaK-type molecula
10	32	57.1	31	A23887	fibrillarin - rat
11	31.5	56.2	40	P00202	endo-1,4-beta-xyla
12	31	55.4	10	F60527	sperm-activating p
13	31	55.4	17	B61321	histone H4 - chick
14	31	55.4	17	A61321	histone H4 - commo
15	31	55.4	20	S68620	histone H4 - sea u
16	31	55.4	23	I51431	histone H4-1 precu
17	31	55.4	24	B43295	histone H4 - alfal
18	31	55.4	34	H87595	hypothetical prote
19	31	55.4	35	A29663	histone H4 - starf
20	31	55.4	39	T12912	hypothetical prote
21	31	55.4	44	B39859	flavocytochrome c
22	31	55.4	49	D88533	5.0K hypothetical
23	31	55.4	50	C88533	hypothetical prote
24	30	53.6	13	S48210	collagen alpha 1(V
25	30	53.6	29	S06854	chorion class B pr
26	30	53.6	35	T04151	probable 1-aminocy
27	30	53.6	46	A45758	hypothetical glucos
28	30	53.6	49	S46908	cell division prot
29	30	53.6	50	S77924	2,4-dichlorophenol

30	29.5	52.7	47	2	T26981	hypothetical prote
31	29	51.8	16	2	A44897	ferradoxin-NADP re
32	29	51.8	33	2	S13863	dihydrolipoamide d
33	29	51.8	42	2	A99578	lipoprotein vsah (
34	29	51.8	43	2	D58213	protamine III - Am
35	29	51.8	43	2	S41388	protein 3a - human
36	29	51.8	45	2	B35156	dihydrolipoamide d
37	29	51.8	47	2	A61384	tracheal mucin gly
38	29	51.8	48	2	AB2090	hypothetical prote
39	28	50.0	10	2	D60787	sperm-activating p
40	28	50.0	10	2	B60588	sperm-activating p
41	28	50.0	10	2	C60588	sperm-activating p
42	28	50.0	10	2	D60527	sperm-activating p
43	28	50.0	10	2	C60527	sperm-activating p
44	28	50.0	10	2	B60527	sperm-activating p
45	28	50.0	10	2	B60788	sperm-activating p
46	28	50.0	12	2	S70337	napin small chain
47	28	50.0	15	2	B56978	collagen alpha 2(X
48	28	50.0	18	2	S09722	2S albumin small c
49	28	50.0	18	2	S09723	hypothetical prote
50	28	50.0	24	2	G64615	hypothetical prote
51	28	50.0	26	2	T15472	T-cell receptor be
52	28	50.0	28	2	S58389	histone H4.2 - Tet
53	28	50.0	31	2	S10360	histone H4.2 - Tet
54	28	50.0	31	2	S10362	histone H4.2 - Tet
55	28	50.0	31	2	S10264	histone H4.2 - Tet
56	28	50.0	31	2	S10268	histone H4.2 - Tet
57	28	50.0	31	2	S10266	histone H4.2 - Tet
58	28	50.0	31	2	S10270	histone H4.2 - Tet
59	28	50.0	31	2	S10272	histone H4.2 - Tet
60	28	50.0	31	2	S10274	histone H4.2 - Tet
61	28	50.0	31	2	S10276	histone H4.2 - Tet
62	28	50.0	31	2	S10278	histone H4.2 - Tet
63	28	50.0	31	2	S10280	histone H4.2 - Tet
64	28	50.0	31	2	S10282	histone H4.2 - Tet
65	28	50.0	31	2	S10284	histone H4.2 - Tet
66	28	50.0	31	2	S10288	histone H4.2 - Tet
67	28	50.0	31	2	S10292	histone H4.2 - Tet
68	28	50.0	31	2	S10294	histone H4.2 - Tet
69	28	50.0	31	2	S10296	histone H4.2 - Tet
70	28	50.0	31	2	S10298	histone H4.2 - Tet
71	28	50.0	31	2	S10300	histone H4.2 - Tet
72	28	50.0	31	2	S10286	histone H4.2 - Tet
73	28	50.0	32	2	S12150	histone H4.2 - Gla
74	28	50.0	33	1	A23483	alcohol oxidase (E
75	28	50.0	37	2	S29113	dipterocin homolog
76	28	50.0	38	2	S55678	calcium-dependent
77	28	50.0	41	2	A58213	protamine - green
78	28	50.0	41	2	S00266	dipterocin B - nes
79	28	50.0	43	2	F83732	hypothetical prote
80	28	50.0	47	2	A58711	variacin precursor
81	27	48.2	10	2	B60589	sperm-activating p
82	27	48.2	15	2	PA0038	protein QA100030 -
83	27	48.2	31	2	D72268	hypothetical prote
84	27	48.2	35	2	A61375	basic fibroblast g
85	27	48.2	37	2	S39367	proteinase omega -
86	27	48.2	38	2	S15845	cathepsin L (EC 3.
87	27	48.2	50	2	AC2221	hypothetical prote
88	26.5	47.3	39	2	G32529	Ig lambda chain v
89	26	46.4	14	2	S47366	T-cell antigen rec
90	26	46.4	17	2	PH0757	T-cell receptor be
91	26	46.4	24	2	F45357	Kex2/subtilisin-li
92	26	46.4	24	2	C45357	Kex2/subtilisin-li
93	26	46.4	26	2	PQ0725	phospholipase A2 (
94	26	46.4	28	2	PH0250	T-cell receptor Vb
95	26	46.4	29	2	S05218	photosystem I 18K
96	26	46.4	30	2	A26188	lipocortin I - pig
97	26	46.4	32	2	S13897	alkaline phosphata
98	26	46.4	33	2	PC2055	lectin - cornucopi
99	26	46.4	34	2	E45357	Kex2/subtilisin-li
100	26	46.4	34	2	B45357	Kex2/subtilisin-li

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:08:33 ; Search time 65.5556 Seconds
(without alignments)
58.997 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GCGGSGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-proc

Database

maximum

database

seq. length

50

P score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	3	Aay97238 Peptide 1
2	56	100.0	10	4	Aae06270 Glycine 1
3	56	100.0	10	4	Ab81034 Linker pe
4	56	100.0	10	4	Ag77866 HLA adapt
5	56	100.0	10	4	Ab31588 Linker us
6	56	100.0	10	5	Abp51822 Fusion pr
7	56	100.0	10	5	Au82114 T-cell sp
8	56	100.0	10	5	Aae25958 Linker pe
9	56	100.0	10	5	Aae23160 Glycine-r
10	56	100.0	10	5	Aae13619 Peptide 1
11	56	100.0	10	6	Aao26601 Fusion pr
12	56	100.0	10	6	Abp56233 Single ch
13	56	100.0	10	6	Abj26727 VEGF bind
14	56	100.0	10	6	Abg72090 pUC19-42K
15	56	100.0	10	6	Abu55753 Polylinke
16	56	100.0	10	6	Aae37749 Linker pe
17	56	100.0	10	7	Adc34708 (Gly4Ser)
18	56	100.0	10	7	Adf69795 M. tuberc
19	56	100.0	10	7	Adf11030 Peptide 1
20	56	100.0	10	7	Adg32335 Peptide 1
21	56	100.0	10	7	Adh73607 Spacer pe
22	56	100.0	10	7	Adi40259 Linker pe
23	56	100.0	10	7	Adl06621 STNFR:IG
24	56	100.0	10	7	Adl06630 hUTNFR:IG
25	56	100.0	10	7	Adsl9142 Peptide 8

26	56	100.0	10	8	ADG47240 Peptide u
27	56	100.0	10	8	Adi82602 Fab elbow
28	56	100.0	10	8	Adk18213 Mouse ant
29	56	100.0	10	8	Adl23305 Linker pe
30	56	100.0	10	8	Adl24299 Cardiovas
31	56	100.0	10	8	Adm98278 (Gly4Ser)
32	56	100.0	10	8	Ado21839 Histone a
33	56	100.0	10	8	Adq59569 Protein f
34	56	100.0	10	8	Adr32306 Linker pe
35	56	100.0	11	2	Aar99242 (Gly4Ser)
36	56	100.0	12	3	Ab25906 Linker se
37	56	100.0	12	3	Aau82047 T-cell sp
38	56	100.0	12	6	Abu9673 INF-beta-
39	56	100.0	12	6	Abp72704 Flexible
40	56	100.0	13	2	Aay43499 Linker fo
41	56	100.0	13	3	Ab29543 Linker pe
42	56	100.0	13	3	Aay44696 Peptide 1
43	56	100.0	13	3	Aay80115 IL-6R and
44	56	100.0	13	3	Aay83213 Peptide 1
45	56	100.0	13	3	Aay83220 Peptide 1
46	56	100.0	13	4	Ab81897 IL6 recep
47	56	100.0	13	6	Abp72701 Flexible
48	56	100.0	14	2	Aar87024 Flexible
49	56	100.0	14	2	Aaw23417 Linker pe
50	56	100.0	14	2	Aaw47355 Polylinke
51	56	100.0	14	2	Aay17953 Amino aci
52	56	100.0	14	2	Aay27115 Linker pe
53	56	100.0	14	2	Aay23638 Linker pe
54	56	100.0	14	3	Ab03812 Polylinke
55	56	100.0	14	3	Aay9938 Peptide u
56	56	100.0	14	4	Aab62063 Sequence
57	56	100.0	14	4	Aay72751 Poly link
58	56	100.0	14	4	Abb56483 Human ain
59	56	100.0	14	6	Abp70843 Linker pe
60	56	100.0	14	6	Aae37748 Linker pe
61	56	100.0	14	8	Adi47373 Plaamid p
62	56	100.0	14	8	Adj88260 Polylinke
63	56	100.0	14	8	Ado49278 Peptide 1
64	56	100.0	14	8	Ado49266 Peptide 1
65	56	100.0	14	8	Adq91247 Interleuk
66	56	100.0	14	8	Adr01303 Polylinke
67	56	100.0	15	2	Aar25983 Peptide m
68	56	100.0	15	2	Aar59501 Hydrophil
69	56	100.0	15	2	Aar59500 Hydrophil
70	56	100.0	15	2	Aar85123 Gene deli
71	56	100.0	15	2	Aar76683 Human ONS
72	56	100.0	15	2	Aar99244 (Gly4Ser)
73	56	100.0	15	2	Aar95067 scFv spac
74	56	100.0	15	2	Aaw09323 Peptide 1
75	56	100.0	15	2	Aay49219 Sequence
76	56	100.0	15	2	Aaw10295 Peptide 1
77	56	100.0	15	2	Aaw35984 Peptide 1
78	56	100.0	15	2	Abb76199 Anti-meso
79	56	100.0	15	2	Aaw87784 Antibody-
80	56	100.0	15	2	Aay43414 Peptide S
81	56	100.0	15	2	Aay33328 E6-sFv pe
82	56	100.0	15	2	Aay03763 Linker pe
83	56	100.0	15	2	Aay21600 EP-919566
84	56	100.0	15	2	Aay27397 Flexible
85	56	100.0	15	2	Aae16564 Peptide 1
86	56	100.0	15	3	Aab29542 Linker pe
87	56	100.0	15	3	Aay99636 (Gly4Ser)
88	56	100.0	15	3	Aay22838 Single ch
89	56	100.0	15	3	Aay70606 Protein e
90	56	100.0	15	3	Aay79551 Linker pe
91	56	100.0	15	3	Aay79552 Linker pe
92	56	100.0	15	3	Aay90826 Linker an
93	56	100.0	15	3	Aab23816 Plaamid p
94	56	100.0	15	3	Aay97237 Peptide 1
95	56	100.0	15	3	Aab15682 Single-ch
96	56	100.0	15	4	Aab70169 Gly/Ser 1
97	56	100.0	15	4	Aab98920 Linker pe
98	56	100.0	15	4	Aae13082 Glycine 1

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:02:08 ; Search time 24.4853 Seconds
(without alignments)
330.752 Million cell updates/sec

Title: US-10-622-108-30
Perfect score: 112
Sequence: 1 GGGGGGGGGGGGGGGGGS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	20	9	US-09-953-321-12
2	112	100.0	20	10	US-09-910-483-96
3	112	100.0	20	10	US-09-967-237-116
4	112	100.0	20	10	US-09-911-261A-21
5	112	100.0	20	10	US-09-969-748C-39
6	112	100.0	20	10	US-09-949-039-57
7	112	100.0	20	14	US-10-112-612-75
8	112	100.0	20	14	US-10-057-408-21
9	112	100.0	20	14	US-10-021-818-7
10	112	100.0	20	14	US-10-072-301-4
11	112	100.0	20	14	US-10-071-866-4
					Sequence 12, Appl
					Sequence 96, Appl
					Sequence 116, Appl
					Sequence 21, Appl
					Sequence 35, Appl
					Sequence 57, Appl
					Sequence 71, Appl
					Sequence 25, Appl
					Sequence 7, Appl
					Sequence 4, Appl

12	112	100.0	20	14	US-10-112-691-75	Sequence 75, Appl
13	112	100.0	20	14	US-10-287-941-1	Sequence 1, Appl
14	112	100.0	20	15	US-10-360-828-4	Sequence 4, Appl
15	112	100.0	20	15	US-10-032-037B-123	Sequence 123, App
16	112	100.0	20	15	US-10-029-988B-123	Sequence 123, App
17	112	100.0	20	15	US-10-032-423A-123	Sequence 123, App
18	112	100.0	20	15	US-10-622-108-30	Sequence 30, Appl
19	112	100.0	20	15	US-10-029-926B-123	Sequence 123, App
20	112	100.0	20	15	US-10-333-487-21	Sequence 21, Appl
21	112	100.0	20	16	US-10-475-540-9	Sequence 9, Appl
22	112	100.0	20	16	US-10-334-235-20	Sequence 20, Appl
23	112	100.0	20	16	US-10-746-149-29	Sequence 29, Appl
24	112	100.0	20	16	US-10-609-019-8	Sequence 8, Appl
25	112	100.0	20	16	US-10-470-387-20	Sequence 20, Appl
26	112	100.0	20	16	US-10-746-943-84	Sequence 84, Appl
27	112	100.0	20	16	US-10-492-729-16	Sequence 16, Appl
28	112	100.0	20	16	US-10-634-740-20	Sequence 20, Appl
29	112	100.0	20	17	US-10-885-235-149	Sequence 149, App
30	112	100.0	20	17	US-10-792-498-31	Sequence 31, Appl
31	112	100.0	20	17	US-10-770-304-5	Sequence 5, Appl
32	112	100.0	20	17	US-10-506-651-20	Sequence 20, Appl
33	112	100.0	20	17	US-10-954-094-149	Sequence 149, App
34	112	100.0	20	18	US-10-988-485-4	Sequence 4, Appl
35	112	100.0	20	18	US-10-792-682-75	Sequence 75, Appl
36	112	100.0	20	18	US-10-787-219A-48	Sequence 48, Appl
37	112	100.0	24	9	US-09-851-271A-12	Sequence 12, Appl
38	112	100.0	24	16	US-10-769-831-17	Sequence 17, Appl
39	112	100.0	24	17	US-10-770-140-17	Sequence 17, Appl
40	112	100.0	25	10	US-09-969-748C-40	Sequence 40, Appl
41	112	100.0	25	10	US-09-949-039-56	Sequence 56, Appl
42	112	100.0	25	13	US-10-081-281-32	Sequence 32, Appl
43	112	100.0	25	14	US-10-013-173-11	Sequence 11, Appl
44	112	100.0	25	14	US-10-150-762-11	Sequence 11, Appl
45	112	100.0	25	14	US-10-244-821-11	Sequence 11, Appl
46	112	100.0	25	14	US-10-261-798-91	Sequence 91, Appl
47	112	100.0	25	16	US-10-769-831-16	Sequence 16, Appl
48	112	100.0	25	16	US-10-634-740-21	Sequence 21, Appl
49	112	100.0	25	17	US-10-770-140-1	Sequence 1, Appl
50	112	100.0	25	17	US-10-770-140-16	Sequence 16, Appl
51	112	100.0	25	17	US-10-770-304-4	Sequence 4, Appl
52	112	100.0	25	17	US-10-506-651-14	Sequence 14, Appl
53	112	100.0	26	16	US-10-846-308-36	Sequence 36, Appl
54	112	100.0	30	10	US-09-833-203-19	Sequence 19, Appl
55	112	100.0	30	16	US-10-492-729-17	Sequence 17, Appl
56	112	100.0	30	16	US-10-634-740-22	Sequence 22, Appl
57	112	100.0	30	17	US-10-792-498-32	Sequence 32, Appl
58	112	100.0	35	14	US-10-013-173-30	Sequence 30, Appl
59	112	100.0	35	14	US-10-150-762-30	Sequence 30, Appl
60	112	100.0	35	14	US-10-244-821-30	Sequence 30, Appl
61	112	100.0	40	13	US-10-081-400-1	Sequence 1, Appl
62	112	100.0	40	14	US-10-005-438-9	Sequence 9, Appl
63	112	100.0	40	15	US-10-257-864A-137	Sequence 137, App
64	112	100.0	40	15	US-10-257-864A-138	Sequence 138, App
65	112	100.0	40	16	US-10-608-710-6	Sequence 6, Appl
66	112	100.0	40	16	US-10-768-873-1	Sequence 1, Appl
67	112	100.0	40	16	US-10-399-585-176	Sequence 176, App
68	112	100.0	40	16	US-10-399-585-177	Sequence 177, App
69	112	100.0	40	16	US-10-645-085A-137	Sequence 137, App
70	112	100.0	40	16	US-10-645-085A-138	Sequence 138, App
71	112	100.0	40	16	US-10-492-729-18	Sequence 18, Appl
72	112	100.0	40	17	US-10-917-899-9	Sequence 9, Appl
73	112	100.0	40	17	US-10-792-498-33	Sequence 33, Appl
74	112	100.0	40	20	US-11-016-189-1	Sequence 1, Appl
75	112	100.0	40	20	US-11-049-853-1	Sequence 1, Appl
76	112	100.0	50	10	US-09-949-039-32	Sequence 32, Appl
77	112	100.0	50	17	US-10-842-054-15	Sequence 15, Appl
78	112	100.0	50	17	US-10-792-498-34	Sequence 34, Appl
79	112	100.0	50	18	US-10-841-819B-31	Sequence 31, Appl
80	112	100.0	60	9	US-09-832-297A-12	Sequence 12, Appl
81	112	100.0	60	10	US-09-833-203-18	Sequence 18, Appl
82	112	100.0	60	17	US-10-506-651-17	Sequence 17, Appl
83	112	100.0	80	17	US-10-842-054-10	Sequence 10, Appl
84	112	100.0	209	15	US-10-449-831A-206	Sequence 206, App

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:57:42 ; Search time 23.8235 Seconds
(without alignments)
429.894 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGGGGGGGGGGGGGGGGGGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	92.9	979	1 RPX1_HUMAN	P22670 homo sapien
2	104	92.9	3703	1 ABE1_HUMAN	O15911 homo sapien
3	103	92.0	738	2 O02402	O02402 pinctada fu
4	102	91.1	592	2 Q9PF60	Q9PF60 xyliella fas
5	100	89.3	118	2 Q9VYS6	Q9VYS6 drosophila
6	100	89.3	207	2 Q43522	Q43522 lycopersico
7	100	89.3	221	2 Q65514	Q65514 arabidopsis
8	100	89.3	255	2 Q9SIH2	Q9SIH2 arabidopsis
9	100	89.3	258	2 Q8XLQ8	Q8XLQ8 clostridium
10	100	89.3	283	2 Q8AVB5	Q8AVB5 xenopus lae
11	100	89.3	288	2 Q7Y1Z0	Q7Y1Z0 oryza sativ
12	100	89.3	447	2 Q73628	Q73628 anolis caro
13	100	89.3	541	2 Q87BZ7	Q87BZ7 xyliella fas
14	100	89.3	551	2 Q7SHG8	Q7SHG8 oryza sativ
15	100	89.3	1868	2 Q9VWP3	Q9VWP3 drosophila
16	99	88.4	318	2 Q38777	Q38777 allium sati
17	98	87.5	266	1 CSS1_RABIT	P06813 o calpain s
18	98	87.5	287	1 Q6GLA3	Q6GLA3 xenopus tro
19	98	87.5	306	1 RALY_HUMAN	Q9UKM9 homo sapien
20	98	87.5	355	2 Q786V6	Q786V6 neurospora
21	98	87.5	440	1 FXGA_CHICK	Q98937 gallus gall
22	98	87.5	465	1 FXD3_MOUSE	Q61060 mus musculu
23	98	87.5	1969	2 Q15763	Q15763 dictyosteli
24	98	87.5	2030	2 Q9VWN8	Q9VWN8 drosophila
25	97	86.6	163	2 Q9SUW7	Q9SUW7 drosophila
26	97	86.6	165	2 Q95UX1	Q95UX1 drosophila
27	97	86.6	166	2 Q95UX0	Q95UX0 drosophila
28	97	86.6	267	2 Q6DI12	Q6DI12 xenopus tro
29	97	86.6	268	1 CSS1_HUMAN	P04632 h calpain s
30	97	86.6	271	2 Q49216	Q49216 oryza sativ
31	97	86.6	272	2 Q49228	Q49228 oryza sativ

32	97	86.6	272	2 Q7E3M4	Q7E3M4 oryza sativ
33	97	86.6	291	2 Q39337	Q39337 brassica na
34	97	86.6	321	2 Q69XV3	Q69XV3 oryza sativ
35	97	86.6	334	2 Q688M5	Q688M5 oryza sativ
36	97	86.6	461	1 GDF7_MOUSE	P43029 mus musculu
37	97	86.6	500	1 P033_HUMAN	P20264 homo sapien
38	97	86.6	673	2 Q653C5	Q653C5 oryza sativ
39	97	86.6	718	2 Q91TR1	Q91TR1 tupaiid her
40	96	85.7	61	2 Q8FUA2	Q8FUA2 xanthomonas
41	96	85.7	72	2 Q8H7A9	Q8H7A9 arabidopsis
42	96	85.7	89	2 Q6ZAB1	Q6ZAB1 oryza sativ
43	96	85.7	93	2 Q6YY22	Q6YY22 oryza sativ
44	96	85.7	104	1 HOL3_HOLDI	Q25055 holotrichia
45	96	85.7	105	2 Q9GNH2	Q9GNH2 drosophila
46	96	85.7	106	2 Q9GF78	Q9GF78 drosophila
47	96	85.7	106	2 Q9GF80	Q9GF80 drosophila
48	96	85.7	106	2 Q7XJP7	Q7XJP7 arabidopsis
49	96	85.7	132	2 Q943G4	Q943G4 oryza sativ
50	96	85.7	136	2 Q18444	Q18444 caenorhabdi
51	96	85.7	155	2 Q9GND8	Q9GND8 drosophila
52	96	85.7	155	2 Q9GF74	Q9GF74 drosophila
53	96	85.7	156	2 Q9GNB7	Q9GNB7 drosophila
54	96	85.7	156	2 Q9GF73	Q9GF73 drosophila
55	96	85.7	157	2 Q9GF77	Q9GF77 drosophila
56	96	85.7	159	2 Q95UW1	Q95UW1 drosophila
57	96	85.7	159	2 Q95UW5	Q95UW5 drosophila
58	96	85.7	161	2 Q95UW6	Q95UW6 drosophila
59	96	85.7	161	2 Q95UX3	Q95UX3 drosophila
60	96	85.7	162	2 Q95UX5	Q95UX5 drosophila
61	96	85.7	163	2 Q95NU6	Q95NU6 drosophila
62	96	85.7	163	2 Q95UW9	Q95UW9 drosophila
63	96	85.7	163	2 Q95UX4	Q95UX4 drosophila
64	96	85.7	164	2 Q95NP2	Q95NP2 drosophila
65	96	85.7	164	2 Q95UW3	Q95UW3 drosophila
66	96	85.7	165	2 Q95NR6	Q95NR6 drosophila
67	96	85.7	165	2 Q95UW2	Q95UW2 drosophila
68	96	85.7	165	2 Q95UX2	Q95UX2 drosophila
69	96	85.7	165	2 Q9GF44	Q9GF44 drosophila
70	96	85.7	167	2 Q9LQ28	Q9LQ28 arabidopsis
71	96	85.7	168	2 Q95UW8	Q95UW8 drosophila
72	96	85.7	175	2 Q9LSN6	Q9LSN6 arabidopsis
73	96	85.7	192	2 Q92P87	Q92P87 rhizobium m
74	96	85.7	220	2 Q8YWF2	Q8YWF2 oryza sativ
75	96	85.7	233	2 Q92NU7	Q92NU7 rhizobium m
76	96	85.7	239	2 Q69T79	Q69T79 oryza sativ
77	96	85.7	281	1 TR2A_MOUSE	Q69F55 mus musculu
78	96	85.7	290	2 Q8VZW4	Q8VZW4 anabaena sp
79	96	85.7	303	1 CHIB_POPTR	P23031 populus tri
80	96	85.7	306	2 Q8Z9T6	Q8Z9T6 oryza sativ
81	96	85.7	329	2 Q85215	Q85215 oryza sativ
82	96	85.7	336	2 Q7Q8W9	Q7Q8W9 anopheles g
83	96	85.7	424	2 Q99N63	Q99N63 mesocricetu
84	96	85.7	443	1 P032_HUMAN	P20265 homo sapien
85	96	85.7	443	1 Q86V54	Q86V54 homo sapien
86	96	85.7	445	1 P032_MOUSE	P31360 mus musculu
87	96	85.7	531	2 Q9BZG5	Q9BZG5 homo sapien
88	96	85.7	539	2 Q9NUA2	Q9NUA2 homo sapien
89	96	85.7	542	2 Q9BZG6	Q9BZG6 homo sapien
90	96	85.7	544	2 Q9BZG7	Q9BZG7 homo sapien
91	96	85.7	683	2 Q7QEL7	Q7QEL7 anopheles g
92	96	85.7	697	2 Q9GRW7	Q9GRW7 drosophila
93	96	85.7	698	2 Q9GRX4	Q9GRX4 drosophila
94	96	85.7	698	2 Q8QKX8	Q8QKX8 ectocarpus
95	96	85.7	919	1 ANDR_HUMAN	P10275 homo sapien
96	96	85.7	1084	2 Q43010	Q43010 oryza sativ
97	96	85.7	1100	2 Q8S064	Q8S064 oryza sativ
98	96	85.7	1309	2 Q8PJM4	Q8PJM4 xanthomonas
99	96	85.7	1334	2 Q8PHD6	Q8PHD6 xanthomonas
100	96	85.7	1504	2 Q7PSM9	Q7PSM9 anopheles g
101	95	84.8	155	2 Q9VZK6	Q9VZK6 drosophila
102	95	84.8	165	1 GRP1_ORYSA	P25074 oryza sativ
103	95	84.8	263	2 Q9VDJ7	Q9VDJ7 drosophila
104	95	84.8	331	1 SHX2_HUMAN	O60902 homo sapien

No.	Score	Match	Length	DB	ID	Description
1	104	92.9	979	2	A35913	regulatory
2	102	91.1	592	2	E87159	endo-1,4-b
3	100	89.3	207	2	T07381	glycine-1
4	100	89.3	221	2	T04592	glycine-
5	100	89.3	255	2	B84777	hypoth
6	100	89.3	2783	1	A41948	alpa
7	98	87.5	266	1	C19EL	calp
8	98	87.5	440	2	E71795	tran
9	98	87.5	1959	2	T08875	'kin
10	97	86.6	151	2	S45296	
11	97	86.6	768	1	C19UL	
12	97	86.6	772	2	T07145	
13	97	86.6	772	2	T07145	
14	97	86.6	772	2	T07145	
15	97	86.6	772	2	T07145	
16	97	86.6	772	2	T07145	
17	97	86.6	772	2	T07145	
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21	97	86.6	772	2	T07145	
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32	97	86.6	772	2	T07145	
33	97	86.6	772	2	T07145	
34	97	86.6	772	2	T07145	
35	97	86.6	772	2	T07145	
36	97	86.6	772	2	T07145	
37	97	86.6	772	2	T07145	
38	97	86.6	772	2	T07145	
39	97	86.6	772	2	T07145	
40	97	86.6	772	2	T07145	
41	97	86.6	772	2	T07145	
42	97	86.6	772	2	T07145	
43	97	86.6	772	2	T07145	
44	97	86.6	772	2	T07145	
45	97	86.6	772	2	T07145	
46	97	86.6	772	2	T07145	
47	97	86.6	772	2	T07145	
48	97	86.6	772	2	T07145	
49	97	86.6	772	2	T07145	
50	97	86.6	772	2	T07145	

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:54:42 ; Search time 26.25 Seconds
(without alignments)
294.675 Million cell updates/sec

Title: US-10-622-108-30

Perfect score: 112

Sequence: 1 GGGGGGGGGGGGGGGGGGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

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1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	20	2	Aar87737 Spacer #5
2	112	100.0	20	2	Aaw18554 Linker se
3	112	100.0	20	2	Aay43415 Peptide S
4	112	100.0	20	3	Aab03035 Flexible
5	112	100.0	20	5	Abp51824 Fusion pr
6	112	100.0	20	5	Abg78248 Human Fv
7	112	100.0	20	5	Aau75147 Linker pe
8	112	100.0	20	5	Aae21140 Linker pe
9	112	100.0	20	5	Abg91939 Human ant
10	112	100.0	20	6	Abr57056 Peptide 1
11	112	100.0	20	6	Aae37194 Linker pe
12	112	100.0	20	6	Abp60059 Flexible
13	112	100.0	20	6	Aag79954 VH-VL lin
14	112	100.0	20	6	Abr62592 Peptide 1
15	112	100.0	20	7	Aae38680 Linker pe
16	112	100.0	20	7	Adc34709 (Ser4Gly)
17	112	100.0	20	7	Adf44885 Anti-CCR5
18	112	100.0	20	7	Adn97318 Linker pe
19	112	100.0	20	7	Adn97316 Linker pe
20	112	100.0	20	8	Adg42781 Peptide 1
21	112	100.0	20	8	Adi04108 Spacer (G
22	112	100.0	20	8	Adm98280 (Gly4Ser)
23	112	100.0	20	8	Ado21851 Histone a
24	112	100.0	20	8	Adg91462 Peptide s
25	112	100.0	20	8	Adt62591 spacer se

26	112	100.0	21	8	ADR49619
27	112	100.0	22	2	AAR87736
28	112	100.0	24	2	AAY23689
29	112	100.0	24	3	AAY94379
30	112	100.0	24	8	ADM95078
31	112	100.0	25	2	AAM18555
32	112	100.0	25	2	AAW10303
33	112	100.0	25	6	ABJ39013
34	112	100.0	25	7	ABU64228
35	112	100.0	25	8	ADM95077
36	112	100.0	25	8	ADO21852
37	112	100.0	25	8	ADQ77071
38	112	100.0	26	8	ADL24301
39	112	100.0	28	2	AAY25360
40	112	100.0	30	4	AAG77868
41	112	100.0	30	6	AAE37195
42	112	100.0	30	6	ADN00801
43	112	100.0	30	8	ADO21853
44	112	100.0	30	8	ADP48740
45	112	100.0	32	3	ABO00160
46	112	100.0	33	2	AAY25359
47	112	100.0	33	3	ABO00157
48	112	100.0	35	6	ABJ39015
49	112	100.0	35	8	ADQ77072
50	112	100.0	39	3	ABO00159
51	112	100.0	40	3	AAY87573
52	112	100.0	40	6	ABU09677
53	112	100.0	40	6	AAE37196
54	112	100.0	40	8	ADQ28273
55	112	100.0	60	4	AAU05183
56	112	100.0	60	4	AAG77867
57	112	100.0	209	8	ADJ36257
58	112	100.0	233	4	ABBS6473
59	112	100.0	234	2	AAW10509
60	112	100.0	239	8	ADJ36245
61	112	100.0	242	8	ADJ36241
62	112	100.0	245	8	ADS78353
63	112	100.0	247	6	AAO27252
64	112	100.0	247	6	AAO27256
65	112	100.0	247	6	AAO27254
66	112	100.0	247	6	AAO27253
67	112	100.0	247	8	ADK42701
68	112	100.0	249	5	ABW75150
69	112	100.0	249	5	ABB78281
70	112	100.0	250	7	ADFA4902
71	112	100.0	250	7	ADFA4910
72	112	100.0	250	7	ADKL7376
73	112	100.0	250	7	ADKL7384
74	112	100.0	250	8	ADG42798
75	112	100.0	250	8	ADG42806
76	112	100.0	252	4	ABBS6469
77	112	100.0	253	7	ADFA4904
78	112	100.0	253	7	ADFA4898
79	112	100.0	253	7	ADFA4912
80	112	100.0	253	7	ADFA4906
81	112	100.0	253	7	ADKL7386
82	112	100.0	253	7	ADKL7380
83	112	100.0	253	7	ADKL7372
84	112	100.0	253	7	ADKL7378
85	112	100.0	253	8	ADG42802
86	112	100.0	253	8	ADG42794
87	112	100.0	253	8	ADG42808
88	112	100.0	253	8	ADG42800
89	112	100.0	254	7	ADFA4900
90	112	100.0	254	7	ADH44196
91	112	100.0	254	7	ADKL7374
92	112	100.0	254	8	ADG42796
93	112	100.0	257	7	ADH44197
94	112	100.0	258	7	ADFA4908
95	112	100.0	258	7	ADKL7382
96	112	100.0	258	8	ADG42804
97	112	100.0	261	7	ADH44201
98	112	100.0	261	7	ADH44199

Adr49619	Human IgG
Aar87736	Spacer #4
Aay23689	Stalling
Aay94379	Zinc fing
Adm95078	Poly-glyc
Aaw18555	Linker se
Aaw10303	Peptide 1
Abj39013	Synthetic
Abu64228	HIV gp 16
Adm95077	Poly-glyc
Ado21852	Histone a
Adq77071	Peptide 1
Adl24301	Cardiovas
Aay25360	IFNAR2/IF
Aag77868	MHC class
Aae37195	Linker pe
Adn00801	Epitope p
Ado21853	Histone a
Adp48740	Linker pe
Aab00160	Linker pe
Aay25359	IFNAR2/IF
Aab00157	Seven rep
Abj39015	Synthetic
Adq77072	Peptide 1
Aab00159	Seven rep
Aay87573	Linker be
Abu09677	INP-beta-
Aae37196	Linker pe
Adq28273	Peptide 1
AAU05183	Pain-rel
Aag77867	MHC class
ADJ36257	Self-coal
ABBS6473	Murine PC
AAW10509	Soluble f
ADJ36245	Self-coal
ADJ36241	Self-coal
ADS78353	TAR1-5-19
AAO27252	Antibody
AAO27256	Antibody
AAO27254	Antibody
AAO27253	Antibody
ADK42701	14B7 scFv
Aau75150	Amino aci
ABB78281	Fluoresce
ADFA4902	Single ch
ADFA4910	Single ch
ADKL7376	Anti-huma
ADKL7384	Anti-huma
ADG42798	Human CCR
ADG42806	Human CCR
ABBS6469	Murine PC
ADFA4904	Single ch
ADFA4898	Single ch
ADFA4912	Single ch
ADFA4906	Single ch
ADKL7386	Anti-huma
ADKL7380	Anti-huma
ADKL7372	Anti-huma
ADKL7378	Anti-huma
ADG42802	Human CCR
ADG42794	Human CCR
ADG42808	Human CCR
ADG42800	Human CCR
ADFA4900	Single ch
ADH44196	sfv antib
ADKL7374	Anti-huma
ADG42796	Human CCR
ADH44197	sfv antib
ADFA4908	Single ch
ADKL7382	Anti-huma
ADG42804	Human CCR
ADH44201	sfv antib
ADH44199	sfv antib

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OM protein - protein search, using sw model

Run on: September 19, 2005, .09:02:08 ; Search time 18.364 Seconds
(without alignments)
330.752 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGSGGGGGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 23: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	9	US-09-767-395-31
2	84	100.0	15	9	US-09-287-849-46
3	84	100.0	15	9	US-09-147-142-29
4	84	100.0	15	9	US-09-782-650-8
5	84	100.0	15	9	US-09-766-543-6
6	84	100.0	15	9	US-09-746-359A-72
7	84	100.0	15	9	US-09-808-037-2
8	84	100.0	15	9	US-09-976-787-17
9	84	100.0	15	9	US-09-911-610-5
10	84	100.0	15	9	US-09-865-198-17
11	84	100.0	15	9	US-09-759-352-45
12	84	100.0	15	9	US-09-767-395-31
13	84	100.0	15	9	US-09-287-849-46
14	84	100.0	15	9	US-09-147-142-29
15	84	100.0	15	9	US-09-782-650-8
16	84	100.0	15	9	US-09-766-543-6
17	84	100.0	15	9	US-09-746-359A-72
18	84	100.0	15	9	US-09-808-037-2
19	84	100.0	15	9	US-09-976-787-17
20	84	100.0	15	9	US-09-911-610-5
21	84	100.0	15	9	US-09-865-198-17
22	84	100.0	15	9	US-09-759-352-45
23	84	100.0	15	9	US-09-767-395-31
24	84	100.0	15	9	US-09-287-849-46
25	84	100.0	15	9	US-09-147-142-29
26	84	100.0	15	9	US-09-782-650-8
27	84	100.0	15	9	US-09-766-543-6
28	84	100.0	15	9	US-09-746-359A-72
29	84	100.0	15	9	US-09-808-037-2
30	84	100.0	15	9	US-09-976-787-17
31	84	100.0	15	9	US-09-911-610-5
32	84	100.0	15	9	US-09-865-198-17
33	84	100.0	15	9	US-09-759-352-45
34	84	100.0	15	9	US-09-767-395-31
35	84	100.0	15	9	US-09-287-849-46
36	84	100.0	15	9	US-09-147-142-29
37	84	100.0	15	9	US-09-782-650-8
38	84	100.0	15	9	US-09-766-543-6
39	84	100.0	15	9	US-09-746-359A-72
40	84	100.0	15	9	US-09-808-037-2
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46	84	100.0	15	9	US-09-287-849-46
47	84	100.0	15	9	US-09-147-142-29
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51	84	100.0	15	9	US-09-808-037-2
52	84	100.0	15	9	US-09-976-787-17
53	84	100.0	15	9	US-09-911-610-5
54	84	100.0	15	9	US-09-865-198-17
55	84	100.0	15	9	US-09-759-352-45
56	84	100.0	15	9	US-09-767-395-31
57	84	100.0	15	9	US-09-287-849-46
58	84	100.0	15	9	US-09-147-142-29
59	84	100.0	15	9	US-09-782-650-8
60	84	100.0	15	9	US-09-766-543-6
61	84	100.0	15	9	US-09-746-359A-72
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97	84	100.0	15	9	US-09-911-610-5
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103	84	100.0	15	9	US-09-782-650-8
104	84	100.0	15	9	US-09-766-543-6
105	84	100.0	15	9	US-09-746-359A-72
106	84	100.0	15	9	US-09-808-037-2
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110	84	100.0	15	9	US-09-759-352-45
111	84	100.0	15	9	US-09-767-395-31
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138	84	100.0	15	9	US-09-746-359A-72
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140	84	100.0	15	9	US-09-976-787-17
141	84	100.0	15	9	US-09-911-610-5
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143	84	100.0	15	9	US-09-759-352-45
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145	84	100.0	15	9	US-09-287-849-46
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147	84	100.0	15	9	US-09-782-650-8
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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:57:42 ; Search time 17.8676 Seconds
(without alignments)
429.894 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGGGGGGGGGGGG 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	170	2	Q925S2
2	84	100.0	240	2	Q652C9
3	84	100.0	241	2	Q921A6
4	84	100.0	243	2	Q7TQM2
5	84	100.0	244	2	Q652C8
6	84	100.0	248	2	Q652Q7
7	84	100.0	255	2	Q6KB05
8	84	100.0	262	2	Q652I1
9	84	100.0	298	2	Q9QYF0
10	84	100.0	487	2	Q652L2
11	84	100.0	738	2	Q02402
12	80	95.2	306	1	RALY HUMAN
13	80	95.2	592	2	Q9PF60
14	79	94.0	104	1	HOL3 HOLDI
15	78	92.9	218	2	Q925S1
16	77	91.7	155	2	Q9VZK6
17	77	91.7	206	1	TWS1 MOUSE
18	76	90.5	80	2	Q8MU97
19	76	90.5	100	2	Q8MU90
20	76	90.5	104	2	Q9GN83
21	76	90.5	104	2	Q9GN84
22	76	90.5	113	2	Q8VY68
23	76	90.5	118	2	Q8VY68
24	76	90.5	119	2	Q7VTS6
25	76	90.5	158	2	Q7VYD8
26	76	90.5	165	1	GRP1 ORYSA
27	76	90.5	175	2	Q9LSN6
28	76	90.5	204	2	Q9WZ47
29	76	90.5	207	2	Q43522
30	76	90.5	221	2	Q65514
31	76	90.5	222	2	Q7XDV2

Q84W21	arabidopsis	227	90.5	76	32	Q84W21
Q7F1E2	oryza sativ	237	90.5	76	33	Q7F1E2
Q9S1H2	arabidopsis	255	90.5	76	34	Q9S1H2
Q8X1Q8	clostridium	258	90.5	76	35	Q8X1Q8
Q9V6A4	drosofila	259	90.5	76	36	Q9V6A4
Q9DFB6	gallus gall	264	90.5	76	37	Q9DFB6
Q7W2S7	bordetella	272	90.5	76	38	Q7W2S7
P29022	zea mays (m	280	90.5	76	39	CHIA MAIZE
Q6JbK8	zea mays (s	280	90.5	76	40	Q6JbK8
Q8AVB5	xenopus lae	283	90.5	76	41	Q8AVB5
Q7Y1Z0	oryza sativ	288	90.5	76	42	Q7Y1Z0
Q8RUS0	arabidopsis	296	90.5	76	43	Q8RUS0
Q7W0G7	bordetella	300	90.5	76	44	Q7W0G7
Q7WDS5	bordetella	304	90.5	76	45	Q7WDS5
P42669	mus musculus	321	90.5	76	46	PUR MOUSE
Q9MYX6	ovis aries	321	90.5	76	47	Q9MYX6
Q00577	homo sapien	322	90.5	76	48	PUR HUMAN
Q7TNS5	mus musculus	333	90.5	76	49	Q7TNS5
Q8C8L2	mus musculus	333	90.5	76	50	Q8C8L2
Q65330	elaeagnus u	335	90.5	76	51	Q65330
Q62376	mus musculus	378	90.5	76	52	RUI17 MOUSE
Q6S9V4	musca domes	397	90.5	76	53	Q6S9V4
Q9W2R6	drosofila	418	90.5	76	54	Q9W2R6
P09026	mus musculus	433	90.5	76	55	HXB3 MOUSE
Q73628	anolis caro	447	90.5	76	56	Q73628
Q8K1I7	mus musculus	493	90.5	76	57	Q8K1I7
Q6S9V3	musca domes	527	90.5	76	58	Q6S9V3
Q13344	homo sapien	528	90.5	76	59	Q13344
Q24563	drosofila	539	90.5	76	60	D0P2 DROME
Q87BZ7	xylella fas	541	90.5	76	61	Q87BZ7
Q75H98	oryza sativ	551	90.5	76	62	Q75H98
Q9VdN4	drosofila	556	90.5	76	63	Q9VdN4
Q67RJ1	homo sapien	581	90.5	76	64	Q67RJ1
Q6PD70	homo sapien	587	90.5	76	65	Q6PD70
Q9hC84	homo sapien	588	90.5	76	66	T7L1 HUMAN
Q0004	canis fami	622	90.5	76	67	SR68 CANFA
Q6NN36	drosofila	638	90.5	76	68	Q6NN36
Q9V121	drosofila	646	90.5	76	69	Q9V121
Q65013	aleutian mi	647	90.5	76	70	Q65013
Q09112	mus musculus	663	90.5	76	71	DUS8 MOUSE
Q7TSZ9	mus musculus	665	90.5	76	72	Q7TSZ9
Q6ZL97	oryza sativ	666	90.5	76	73	Q6ZL97
Q54939	mus musculus	688	90.5	76	74	ROMD MOUSE
Q9J1J1	mus musculus	688	90.5	76	75	Q9J1J1
Q9GRX4	drosofila	698	90.5	76	76	Q9GRX4
Q69Z36	mus musculus	702	90.5	76	77	Q69Z36
Q96608	aleutian mi	702	90.5	76	78	Q96608
Q8bn22	mus musculus	702	90.5	76	79	Q8bn22
Q91tr1	tupalid her	718	90.5	76	80	Q91tr1
Q9V5M5	drosofila	757	90.5	76	81	Q9V5M5
Q6NP15	drosofila	939	90.5	76	82	Q6NP15
Q632Y0	mus musculus	948	90.5	76	83	Q632Y0
P22870	homo sapien	979	90.5	76	84	RPX1 HUMAN
Q86P20	drosofila	987	90.5	76	85	Q86P20
Q93197	bordetella	1039	90.5	76	86	Q93197
Q7KV88	drosofila	1102	90.5	76	87	Q7KV88
Q7PKP4	anopheles g	1198	90.5	76	88	Q7PKP4
Q7KV90	drosofila	1200	90.5	76	89	Q7KV90
Q9W3Q5	drosofila	1255	90.5	76	90	Q9W3Q5
Q95PH4	dicyostell	1318	90.5	76	91	Q95PH4
Q9W002	drosofila	1504	90.5	76	92	Q9W002
TP2B	CHICK	1627	90.5	76	93	TP2B CHICK
Q9VWP3	gallus gall	1868	90.5	76	94	Q9VWP3
Q81ZY8	homo sapien	1957	90.5	76	95	Q81ZY8
Q15763	dicyostell	1969	90.5	76	96	Q15763
Q8nrd5	homo sapien	2165	90.5	76	97	Q8nrd5
Q15111	homo sapien	3703	90.5	76	98	ABF1 HUMAN
Q61329	mus musculus	3726	90.5	76	99	ABF1 MOUSE
Q98109	arabidopsis	302	89.3	75	100	Q98109
Q38777	allium sati	318	89.3	75	101	Q38777
Q65517	arabidopsis	322	89.3	75	102	Q65517
Q90WR5	lampetra fl	629	89.3	75	103	Q90WR5
Q22872	caenorhabdi	790	89.3	75	104	Q22872

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:58:27 ; Search time 3.75 Seconds
(without alignments)
384.867 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGGGGGGGGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	95.2	592	2 E82759	endo-1,4-beta-gluc
2	79	94.0	104	2 JC4190	holotricin 3 precu
3	78	92.9	249	2 S41374	single chain Fv an
4	77	91.7	206	2 I53066	gene M-twist prote
5	77	91.7	268	2 A56446	Ig heavy chain V r
6	76	90.5	80	2 T10550	hypothetical prote
7	76	90.5	165	1 KNR2G1	glycine-rich cell
8	76	90.5	207	2 T07381	glycine-rich prote
9	76	90.5	221	2 T04592	glycine-rich cell
10	76	90.5	255	2 B84777	hypothetical prote
11	76	90.5	280	2 A42424	chitinase (EC 3.2.
12	76	90.5	322	2 A45036	single-stranded-DN
13	76	90.5	378	2 S04336	U1 snRNP 70K prote
14	76	90.5	433	2 S20963	homeotic protein H
15	76	90.5	528	2 G02127	fus-like protein -
16	76	90.5	979	2 A35913	regulatory factor
17	76	90.5	1969	2 T08875	histidine kinase h
18	76	90.5	2783	1 A41948	alpha-fetoprotein
19	75	89.3	302	2 C84470	hypothetical prote
20	75	89.3	322	2 T04595	hypothetical prote
21	75	89.3	1226	2 T24045	hypothetical prote
22	74	88.1	266	1 CIRBL	calpain (EC 3.4.22
23	74	88.1	440	2 S71795	transcription fact
24	74	88.1	722	1 VCPVW2	coat protein VP1 -
25	74	88.1	877	2 T43449	hypothetical prote
26	74	88.1	895	2 JC7089	zinc finger bindin
27	73	86.9	151	2 S43296	bone morphogenetic
28	73	86.9	211	2 T04098	CBP20 preproprotei
29	73	86.9	263	2 A34466	calpain (EC 3.4.22

30	73	86.9	266	1 CIPGL	calpain (EC 3.4.22
31	73	86.9	268	1 CIRHL	calpain (EC 3.4.22
32	73	86.9	272	2 T02745	nucleic acid bindi
33	73	86.9	291	1 S31415	glycine-rich prote
34	73	86.9	333	2 A39065	homeotic protein E
35	73	86.9	367	2 JC6087	helix-loop-helix t
36	73	86.9	377	2 T04213	heat shock transcr
37	73	86.9	396	2 T49109	glycine-rich prote
38	73	86.9	495	1 S31223	transcription fact
39	73	86.9	681	2 AB2155	hypothetical prote
40	73	86.9	901	2 JC6093	dead ringer nuclea
41	73	86.9	1473	2 T13855	suppressor of sabl
42	72	85.7	106	2 F84797	hypothetical prote
43	72	85.7	113	2 S44750	C06G4.3 protein -
44	72	85.7	136	2 T29282	hypothetical prote
45	72	85.7	188	2 S49192	GCR 1 protein - fr
46	72	85.7	199	2 S16063	acp-22 protein - y
47	72	85.7	199	2 S32224	acp-22 protein - y
48	72	85.7	220	2 A4805	eggshell protein p
49	72	85.7	270	2 T35365	hypothetical prote
50	72	85.7	273	2 T51145	nucleic acid bindi
51	72	85.7	290	2 AD1849	hypothetical prote
52	72	85.7	336	1 S18750	chitinase (EC 3.2.
53	72	85.7	384	1 A26099	glycine-rich cell
54	72	85.7	384	2 D86448	RNA-binding protei
55	72	85.7	404	2 S54729	gene Brn-3b protei
56	72	85.7	410	2 T38502	Brn-3 - mouse
57	72	85.7	411	2 I58156	hypothetical prote
58	72	85.7	435	2 T15143	transcription fact
59	72	85.7	443	1 S29334	transcription fact
60	72	85.7	445	1 A49447	transcription fact
61	72	85.7	445	1 S31224	hypothetical prote
62	72	85.7	586	2 T26667	hypothetical prote
63	72	85.7	587	1 B4276	coat protein VP1 -
64	72	85.7	702	1 VCPVAP	coat protein VP1 -
65	72	85.7	716	1 VCPV2M	coat protein VP1 -
66	72	85.7	718	1 VCPVIM	androgen receptor
67	72	85.7	910	2 A34721	androgen receptor
68	72	85.7	911	2 B34721	androgen receptor
69	72	85.7	919	2 A39248	androgen receptor
70	72	85.7	1084	2 T04103	sucrose-phosphate
71	71	84.5	162	2 C85356	glycine-rich prote
72	71	84.5	271	2 S34666	glycine-rich prote
73	71	84.5	321	2 A38712	fibillarlin [valid
74	71	84.5	393	2 T20268	hypothetical prote
75	71	84.5	427	2 A32372	female-specific do
76	71	84.5	465	2 G02738	FRAC-4 - human
77	71	84.5	475	2 A43915	homeotic protein e
78	71	84.5	549	2 B32372	male-specific doub
79	71	84.5	664	2 JC7990	acetylcholinestera
80	71	84.5	1276	2 E96776	hypothetical prote
81	71	84.5	1433	2 A46053	bulbous pemphigoid
82	71	84.5	1664	2 T18262	S-layer protein -
83	70	83.3	139	2 S31443	glycine-rich RNA-b
84	70	83.3	158	2 T05254	probable RNA-bindi
85	70	83.3	171	2 H84709	probable glycine-r
86	70	83.3	233	2 JC5322	p53 specific singl
87	70	83.3	238	2 T05344	hypothetical prote
88	70	83.3	252	1 S01821	glycine-rich prote
89	70	83.3	259	2 T15126	hypothetical prote
90	70	83.3	268	2 S09860	hypothetical prote
91	70	83.3	284	2 S74256	homeotic protein s
92	70	83.3	330	2 S74255	homeotic protein s
93	70	83.3	331	2 S78452	POU-domain protein
94	70	83.3	420	2 I59234	octamer binding tr
95	70	83.3	420	2 A49642	transcription fact
96	70	83.3	431	1 WJHU2G	homeotic protein H
97	70	83.3	448	2 T15188	hypothetical prote
98	70	83.3	500	2 T22068	hypothetical prote
99	70	83.3	616	2 A58947	signal recognition
100	70	83.3	892	2 T27005	hypothetical prote
101	70	83.3	1102	2 JC6316	probable protein k
102	69.5	82.7	243	2 T46231	PRE-MRNA SPLICING

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:54:42 ; Search time 19.6875 Seconds
(without alignments)
294.675 Million cell updates/sec

Title: US-10-622-108-29

Perfect score: 84

Sequence: 1 GGGSGGGSGGGGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	2 AAR25983	Aar25983 Peptide m
2	84	100.0	15	2 AAR59500	Aar59500 Hydrophil
3	84	100.0	15	2 AAR85123	Aar85123 Gene deli
4	84	100.0	15	2 AAR76683	Aar76683 Human ONS
5	84	100.0	15	2 AAR99244	Aar99244 (Gly4Ser)
6	84	100.0	15	2 AAR95067	Aar95067 scFv spac
7	84	100.0	15	2 AAW09323	Aaw09323 Peptide 1
8	84	100.0	15	2 AAY49219	Aay49219 Sequence
9	84	100.0	15	2 AAW10295	Aaw10295 Peptide 1
10	84	100.0	15	2 AAW35984	Aaw35984 Peptide 1
11	84	100.0	15	2 AAW87784	Aaw87784 Antibody-
12	84	100.0	15	2 AAY43414	Aay43414 Peptide S
13	84	100.0	15	2 AAY33328	Aay33328 E6-sfv pe
14	84	100.0	15	2 AAY03763	Aay03763 Linker pe
15	84	100.0	15	2 AAY21600	Aay21600 EP-919566
16	84	100.0	15	2 AAY27397	Aay27397 Flexible
17	84	100.0	15	2 AAE15564	Aae15564 Peptide 1
18	84	100.0	15	3 AAB29542	Aab29542 Linker pe
19	84	100.0	15	3 AAY99636	Aay99636 (Gly4Ser)
20	84	100.0	15	3 AAB22838	Aab22838 Single ch
21	84	100.0	15	3 AAY70606	Aay70606 Protein e
22	84	100.0	15	3 AAY79551	Aay79551 Linker pe
23	84	100.0	15	3 AAY79552	Aay79552 Linker pe
24	84	100.0	15	3 AAY90826	Aay90826 Linker am
25	84	100.0	15	3 AAB23816	Aab23816 Plasmid p

26	84	100.0	15	3 AAY97237	Aay97237 Peptide 1
27	84	100.0	15	3 AAB15682	Aab15682 Single-ch
28	84	100.0	15	4 AAB70169	Aab70169 Gly/Ser 1
29	84	100.0	15	4 AAB98920	Aab98920 Linker pe
30	84	100.0	15	4 AAE13082	Aae13082 Glycine 1
31	84	100.0	15	4 AAM52571	Aam52571 Peptide 1
32	84	100.0	15	4 AAE12408	Aae12408 Peptide 1
33	84	100.0	15	4 AAU08689	Aau08689 Antibody
34	84	100.0	15	4 AAE06268	Aae06268 Glycine 1
35	84	100.0	15	4 AAU09970	Aau09970 Glycine-S
36	84	100.0	15	4 AAU04948	Aau04948 Humanised
37	84	100.0	15	4 AAE13100	Aae13100 Linker pe
38	84	100.0	15	4 ABB79010	Abb79010 Peptide 1
39	84	100.0	15	4 AAB97229	Aab97229 Immunoglo
40	84	100.0	15	4 AAB85296	Aab85296 Sequence
41	84	100.0	15	4 AAU29009	Aau29009 Tumour-sp
42	84	100.0	15	4 AAB58601	Aab58601 Peptide e
43	84	100.0	15	4 AAB48032	Aab48032 Gly-Ser p
44	84	100.0	15	4 AAB61572	Aab61572 Flexible
45	84	100.0	15	4 AAB74579	Aab74579 Context-d
46	84	100.0	15	5 ABG67227	Abg67227 Interleuk
47	84	100.0	15	5 ABP51823	Abp51823 Fusion pr
48	84	100.0	15	5 AAU86039	Aau86039 Human glu
49	84	100.0	15	5 AAU82112	Aau82112 T-cell sp
50	84	100.0	15	5 AAE28918	Aae28918 Peptide 1
51	84	100.0	15	5 AAU11449	Aau11449 Synthetic
52	84	100.0	15	5 AAE23425	Aae23425 Linker pe
53	84	100.0	15	5 ABB98375	Abb98375 Human VEG
54	84	100.0	15	5 AAE18134	Aae18134 Peptide u
55	84	100.0	15	5 ABB84084	Abb84084 Human scd
56	84	100.0	15	5 ABG78249	Abg78249 Human Fv
57	84	100.0	15	5 AAM47630	Aam47630 Linker se
58	84	100.0	15	5 ABP53557	Abp53557 Peptide 1
59	84	100.0	15	5 ABG63325	Abg63325 Synthetic
60	84	100.0	15	5 ABB79500	Abb79500 Peptide 1
61	84	100.0	15	5 AAU99371	Aau99371 Peptide 1
62	84	100.0	15	5 AAE25957	Aae25957 Linker pe
63	84	100.0	15	5 ABG97825	Abg97825 Gly-Ser 1
64	84	100.0	15	5 ABG97807	Abg97807 Synthetic
65	84	100.0	15	5 ABG68874	Abg68874 GGGGS lin
66	84	100.0	15	5 ABG73658	Abg73658 hdm2-asso
67	84	100.0	15	5 ABG35328	Abg35328 Thrombopo
68	84	100.0	15	5 ABG35310	Abg35310 Thrombopo
69	84	100.0	15	5 AAE29080	Aae29080 Linker pe
70	84	100.0	15	5 AAE22203	Aae22203 Peptide 1
71	84	100.0	15	5 AAU75757	Aau75757 Peptide 1
72	84	100.0	15	5 ABG77165	Abg77165 Flexible
73	84	100.0	15	5 ABG31061	Abg31061 Angiogene
74	84	100.0	15	5 AAU76997	Aau76997 Immunoglo
75	84	100.0	15	5 AAU80037	Aau80037 Spacer pe
76	84	100.0	15	5 AAO22077	Aao22077 15 amino
77	84	100.0	15	5 ABG31940	Abg31940 Human ant
78	84	100.0	15	5 ABG32859	Abg32859 Linker pe
79	84	100.0	15	5 AAU75385	Aau75385 Immunotox
80	84	100.0	15	5 AAU75398	Aau75398 Immunotox
81	84	100.0	15	5 ABG32899	Abg32899 Peptide 1
82	84	100.0	15	6 ABU11014	Abu11014 Synthetic
83	84	100.0	15	6 AAO26602	Aao26602 Fusion pr
84	84	100.0	15	6 AAO16063	Aao16063 Neurologi
85	84	100.0	15	6 ABP56234	Abp56234 Single ch
86	84	100.0	15	6 AAE36052	Aae36052 Single ch
87	84	100.0	15	6 ABU08978	Abu08978 (G4S) 3 sp
88	84	100.0	15	6 ABU26809	Abu26809 VEGF bind
89	84	100.0	15	6 ABJ26726	Abj26726 VEGF bind
90	84	100.0	15	6 ABR42598	Abr42598 Peptide 1
91	84	100.0	15	6 AAE37114	Aae37114 Linker pe
92	84	100.0	15	6 ABR55699	Abr55699 Linker pe
93	84	100.0	15	6 ABJ19272	Abj19272 Anti-huma
94	84	100.0	15	6 ABP97415	Abp97415 E487-deri
95	84	100.0	15	6 AAE30958	Aae30958 Linker pe
96	84	100.0	15	6 AAE30956	Aae30956 Linker pe
97	84	100.0	15	6 ABG72723	Abg72723 Linker pe
98	84	100.0	15	6 ABO23257	Abo23257 Light cha

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OM protein - protein search, using sw model

Run on: September 19, 2005, 09:02:08 ; Search time 12.2426 Seconds
(without alignments)
330.752 Million cell updates/sec

Title: US-10-622-108-28
Perfect score: 56
Sequence: 1 GGGGSGGGGS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 segs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	9	US-09-789-522-5
2	56	100.0	10	9	US-09-287-849-45
3	56	100.0	10	9	US-09-147-142-30
4	56	100.0	10	9	US-09-976-787-19
5	56	100.0	10	9	US-09-865-198-19
6	56	100.0	10	9	US-09-790-317-6
7	56	100.0	10	10	US-09-798-689-19
8	56	100.0	10	10	US-09-984-010-16
9	56	100.0	10	10	US-09-949-039-36
10	56	100.0	10	10	US-09-833-203-7
11	56	100.0	10	13	US-10-115-984-7
					Sequence 5, Appli
					Sequence 45, Appl
					Sequence 30, Appl
					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 6, Appli
					Sequence 19, Appl
					Sequence 16, Appl
					Sequence 36, Appl
					Sequence 7, Appli
					Sequence 7, Appli

12	56	100.0	10	14	US-10-082-671-7	Sequence 7, Appli
13	56	100.0	10	14	US-10-282-121-4	Sequence 4, Appli
14	56	100.0	10	14	US-10-252-408-29	Sequence 29, Appl
15	56	100.0	10	14	US-10-021-818-5	Sequence 5, Appli
16	56	100.0	10	14	US-10-288-250-8	Sequence 8, Appli
17	56	100.0	10	14	US-10-262-828A-5	Sequence 5, Appli
18	56	100.0	10	14	US-10-359-460-45	Sequence 45, Appl
19	56	100.0	10	15	US-10-359-459-9	Sequence 9, Appli
20	56	100.0	10	15	US-10-296-317-96	Sequence 96, Appl
21	56	100.0	10	15	US-10-622-108-28	Sequence 28, Appl
22	56	100.0	10	15	US-10-367-956-30	Sequence 30, Appl
23	56	100.0	10	15	US-10-645-000-18	Sequence 18, Appl
24	56	100.0	10	16	US-10-666-871-17	Sequence 17, Appl
25	56	100.0	10	16	US-10-666-886-17	Sequence 17, Appl
26	56	100.0	10	16	US-10-646-308-34	Sequence 34, Appl
27	56	100.0	10	16	US-10-724-178-19	Sequence 19, Appl
28	56	100.0	10	16	US-10-666-898-17	Sequence 17, Appl
29	56	100.0	10	16	US-10-666-834-17	Sequence 17, Appl
30	56	100.0	10	16	US-10-772-021-1	Sequence 1, Appli
31	56	100.0	10	16	US-10-667-193-17	Sequence 17, Appl
32	56	100.0	10	16	US-10-667-166-17	Sequence 17, Appl
33	56	100.0	10	16	US-10-666-833-17	Sequence 17, Appl
34	56	100.0	10	16	US-10-482-630-19	Sequence 19, Appl
35	56	100.0	10	16	US-10-778-910-19	Sequence 19, Appl
36	56	100.0	10	16	US-10-634-740-8	Sequence 8, Appli
37	56	100.0	10	17	US-10-885-225-147	Sequence 147, App
38	56	100.0	10	17	US-10-495-491-10	Sequence 10, Appl
39	56	100.0	10	17	US-10-668-073-17	Sequence 17, Appl
40	56	100.0	10	17	US-10-792-498-30	Sequence 30, Appl
41	56	100.0	10	17	US-10-954-094-147	Sequence 147, App
42	56	100.0	11	13	US-10-115-817-5	Sequence 5, Appli
43	56	100.0	11	14	US-10-247-954-5	Sequence 5, Appli
44	56	100.0	12	13	US-10-081-281-38	Sequence 38, Appl
45	56	100.0	12	14	US-10-005-438-5	Sequence 5, Appli
46	56	100.0	12	15	US-10-296-317-29	Sequence 29, Appl
47	56	100.0	12	17	US-10-917-899-5	Sequence 5, Appli
48	56	100.0	12	17	US-10-485-545A-2	Sequence 2, Appli
49	56	100.0	13	9	US-09-359-672-4	Sequence 4, Appli
50	56	100.0	13	16	US-10-806-422-60	Sequence 60, Appl
51	56	100.0	13	17	US-10-485-545A-15	Sequence 15, Appl
52	56	100.0	14	9	US-09-815-837-108	Sequence 108, App
53	56	100.0	14	9	US-09-766-378A-29	Sequence 29, Appl
54	56	100.0	14	9	US-09-850-715-16	Sequence 16, Appl
55	56	100.0	14	14	US-10-232-838-20	Sequence 20, Appl
56	56	100.0	14	15	US-10-247-839-89	Sequence 89, Appl
57	56	100.0	14	15	US-10-247-839-101	Sequence 101, App
58	56	100.0	14	15	US-10-621-693-61	Sequence 61, Appl
59	56	100.0	14	16	US-10-742-161-5	Sequence 5, Appli
60	56	100.0	14	16	US-10-742-372-5	Sequence 5, Appli
61	56	100.0	15	9	US-09-767-395-31	Sequence 31, Appl
62	56	100.0	15	9	US-09-287-849-46	Sequence 46, Appl
63	56	100.0	15	9	US-09-147-142-29	Sequence 29, Appl
64	56	100.0	15	9	US-09-782-650-8	Sequence 8, Appli
65	56	100.0	15	9	US-09-766-543-6	Sequence 6, Appli
66	56	100.0	15	9	US-09-746-359A-72	Sequence 72, Appl
67	56	100.0	15	9	US-09-808-037-2	Sequence 2, Appli
68	56	100.0	15	9	US-09-976-787-17	Sequence 17, Appl
69	56	100.0	15	9	US-09-911-610-5	Sequence 5, Appli
70	56	100.0	15	9	US-09-865-198-17	Sequence 17, Appl
71	56	100.0	15	9	US-09-759-352-45	Sequence 45, Appl
72	56	100.0	15	9	US-09-867-262-4	Sequence 4, Appli
73	56	100.0	15	9	US-09-747-669-7	Sequence 7, Appli
74	56	100.0	15	9	US-09-987-456-6	Sequence 6, Appli
75	56	100.0	15	9	US-09-987-456-7	Sequence 7, Appli
76	56	100.0	15	9	US-09-753-126-23	Sequence 23, Appl
77	56	100.0	15	9	US-09-885-551A-4	Sequence 4, Appli
78	56	100.0	15	9	US-09-990-205-5	Sequence 5, Appli
79	56	100.0	15	9	US-09-144-886-1	Sequence 1, Appli
80	56	100.0	15	9	US-09-956-206A-67	Sequence 67, Appl
81	56	100.0	15	9	US-09-968-561A-6	Sequence 6, Appli
82	56	100.0	15	9	US-09-887-853-7	Sequence 7, Appli
83	56	100.0	15	10	US-09-939-769-96	Sequence 96, Appl
84	56	100.0	15	10	US-09-749-873-111	Sequence 111, App

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:57:42 ; Search time 11.9118 Seconds
(without alignments)
429.894 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGGGGGGGG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	104	1	HOL3_HOLD1
2	56	100.0	170	2	Q925S2
3	56	100.0	174	2	Q6UIP2
4	56	100.0	218	2	Q925S1
5	56	100.0	240	2	Q652C9
6	56	100.0	241	2	Q921A6
7	56	100.0	243	2	Q7TQM2
8	56	100.0	244	2	Q652C8
9	56	100.0	248	2	Q652D7
10	56	100.0	255	2	Q9V3W7
11	56	100.0	255	2	Q6KB05
12	56	100.0	262	2	Q652I1
13	56	100.0	298	2	Q9QYF0
14	56	100.0	306	1	RALY_HUMAN
15	56	100.0	380	2	Q8T3T5
16	56	100.0	410	2	Q9H7F2
17	56	100.0	487	2	Q652L2
18	56	100.0	489	2	Q7PRW5
19	56	100.0	571	2	Q9VUD3
20	56	100.0	592	2	Q9PP60
21	56	100.0	613	2	Q6ZPM6
22	56	100.0	627	1	SR68_HUMAN
23	56	100.0	683	2	Q7QEL7
24	56	100.0	738	2	Q02402
25	56	100.0	753	1	CNO3_HUMAN
26	56	100.0	896	2	Q96SF0
27	56	100.0	1040	1	PC10_HUMAN
28	53	94.6	158	2	Q851X4
29	53	94.6	201	1	TWS1_PANTR
30	53	94.6	203	2	Q8MI06
31	53	94.6	264	1	GSHI_HUMAN

32	53	94.6	268	2	Q9FIQ2	Q9fiq2 arabidopsis
33	53	94.6	269	1	CHIB_MAIZE	P29023 zea mays (m
34	53	94.6	278	2	Q6JBP7	Q6jbp7 zea diplope
35	53	94.6	280	2	Q6JBQ2	Q6jbq2 zea mays (s
36	53	94.6	280	2	Q6JBQ7	Q6jbq7 zea mays (s
37	53	94.6	282	2	Q6JBQ3	Q6jbq3 zea mays (s
38	53	94.6	282	2	Q6JBQ6	Q6jbq6 zea mays (s
39	53	94.6	290	2	Q7Y2I8	Q7y2i8 arabidopsis
40	53	94.6	304	2	Q7XJ17	Q7xj17 lycopersico
41	53	94.6	401	2	Q7KU81	Q7ku81 drosophila
42	53	94.6	411	1	MBD2_HUMAN	Q8ubbs homo sapien
43	53	94.6	424	2	O87264	O87264 pseudomonas
44	53	94.6	424	2	Q7C4I5	Q7c4i5 pseudomonas
45	53	94.6	435	2	Q8R205	Q8r205 m expressed
46	53	94.6	465	1	FXD1_HUMAN	Q16676 homo sapien
47	53	94.6	476	2	Q7ZXD8	Q7zxd8 xenopus lae
48	53	94.6	478	2	Q7S8J6	Q7s8j6 neurospora
49	53	94.6	488	2	Q9WJF6	Q9wjf6 drosophila
50	53	94.6	560	2	Q7QJF8	Q7qjps anopheles g
51	53	94.6	642	2	Q9PUD8	Q9pud8 lampetra fl
52	53	94.6	687	2	Q9PUD9	Q9pud9 lampetra fl
53	53	94.6	717	2	Q8CHW4	Q8chw4 mus musculu
54	53	94.6	748	2	Q95TS0	Q9ste0 drosophila
55	53	94.6	762	2	Q9VXQ6	Q9vxq6 drosophila
56	53	94.6	1131	2	Q7RWF1	Q7rwl1 neurospora
57	53	94.6	1218	2	Q9W201	Q9w201 drosophila
58	53	94.6	2946	1	NBEA_HUMAN	Q8nf9p homo sapien
59	53	94.6	3038	1	TRIO_HUMAN	Q75962 homo sapien
60	52	92.9	53	2	Q7S2G8	Q7s2g8 neurospora
61	52	92.9	69	1	MCBA_ECOLI	P05834 escherichia
62	52	92.9	69	2	Q7F8S9	Q7f8s9 oryza sativ
63	52	92.9	80	2	Q9SUF7	Q9suf7 arabidopsis
64	52	92.9	87	2	Q9LRI5	Q9lri5 pisum sativ
65	52	92.9	100	2	Q8MU90	Q8mu90 oncopeltus
66	52	92.9	104	2	Q9GN83	Q9gn83 drosophila
67	52	92.9	104	2	Q9GN84	Q9gn84 drosophila
68	52	92.9	104	2	Q9GP72	Q9gp72 drosophila
69	52	92.9	113	2	Q8VY68	Q8vy68 arabidopsis
70	52	92.9	118	2	Q9VYS6	Q9vy68 drosophila
71	52	92.9	119	2	Q7SCN2	Q7scn2 neurospora
72	52	92.9	136	2	Q6RI30	Q6ri30 hepatopancr
73	52	92.9	138	2	Q6RI29	Q6ri29 hepatopancr
74	52	92.9	144	2	Q6KGF4	Q6kgf4 oryza sativ
75	52	92.9	150	2	Q7X243	Q7x243 citrobacter
76	52	92.9	154	2	Q6Z5C4	Q6z5c4 oryza sativ
77	52	92.9	155	2	Q9VZK6	Q9vzk6 drosophila
78	52	92.9	155	2	Q80WU5	Q80wu5 mus musculu
79	52	92.9	157	2	Q70T18	Q70t18 homo sapien
80	52	92.9	158	2	Q9VYD8	Q9vyd8 drosophila
81	52	92.9	159	2	Q67IU2	Q67iu2 oryza sativ
82	52	92.9	159	2	Q9S9Q2	Q9s9q2 arabidopsis
83	52	92.9	160	2	Q69WH5	Q69wh5 oryza sativ
84	52	92.9	162	2	Q6NM15	Q6nm15 arabidopsis
85	52	92.9	164	2	Q7XDT8	Q7xdt8 oryza sativ
86	52	92.9	165	1	GRP1_ORYSA	P25074 oryza sativ
87	52	92.9	175	2	Q9LSN6	Q9lsn6 arabidopsis
88	52	92.9	181	2	Q35328	Q35328 mus musculu
89	52	92.9	185	2	Q948R3	Q948r3 oryza sativ
90	52	92.9	185	2	Q7XDT5	Q7xdt5 oryza sativ
91	52	92.9	185	2	Q7XDT6	Q7xdt6 oryza sativ
92	52	92.9	186	2	Q6I6X8	Q6i6x8 oryza lat
93	52	92.9	188	2	Q6KF83	Q6kf83 hevea brasl
94	52	92.9	192	1	VG49_BPMD2	O64239 mycobacteri
95	52	92.9	194	2	Q8I7W6	Q8i7w6 drosophila
96	52	92.9	194	2	Q9W1I6	Q9w1i6 anopheles g
97	52	92.9	201	2	Q7PHE9	Q7phe9 anopheles g
98	52	92.9	204	2	Q9W2A7	Q9w2a7 drosophila
99	52	92.9	204	2	Q8WC86	Q8wc86 bradyrhizob
100	52	92.9	206	1	TWS1_MOUSE	P26687 mus musculu
101	52	92.9	207	2	Q8MIH8	Q8mih8 cebus capuc
102	52	92.9	207	2	Q43522	Q43522 lycopersico
103	52	92.9	211	2	Q6IQ22	Q6iq22 homo sapien
104	52	92.9	212	2	Q949F9	Q949f9 oryza sativ

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:58:27 ; Search time 2.5 Seconds
(without alignments)
384.867 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGSGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	104	JC4190	holotricin 3 precu
2	56	100.0	249	S41374	single chain Fv an
3	56	100.0	571	T43456	hypothetical prote
4	56	100.0	592	E82759	endo-1,4-beta-gluc
5	53	94.6	268	B42424	chitinase (EC 3.2.
6	53	94.6	465	G02738	PREAC-4 - human
7	52	92.9	69	MIETC77	microcin B17 precu
8	52	92.9	80	T10550	hypothetical prote
9	52	92.9	100	T49621	hypothetical prote
10	52	92.9	159	F86429	protein F26G16.9 (
11	52	92.9	165	1 KNRZG1	glycine-rich cell
12	52	92.9	192	T72805	gp49 protein - Myc
13	52	92.9	206	I53066	Gene M-twist prote
14	52	92.9	207	T07381	Glycine-rich prote
15	52	92.9	212	A83680	spore germination
16	52	92.9	221	T04592	glycine-rich cell
17	52	92.9	224	T51742	RNA helicase RH11
18	52	92.9	238	T05344	hypothetical prote
19	52	92.9	252	1 S01821	hypothetical prote
20	52	92.9	255	B84777	hypothetical prote
21	52	92.9	256	T03371	Glycine-rich prote
22	52	92.9	280	T42424	chitinase (EC 3.2.
23	52	92.9	288	F48423	homeotic protein e
24	52	92.9	291	1 S31415	glycine-rich prote
25	52	92.9	302	T08470	hypothetical prote
26	52	92.9	321	1 S13550	anther-specific pr
27	52	92.9	322	T445036	single-stranded-DN
28	52	92.9	330	T02525	probable DOF zinc
29	52	92.9	339	2 S20880	homeotic protein H

30	52	92.9	341	2 C83578	hypothetical prote
31	52	92.9	367	2 JC6087	helix-loop-helix t
32	52	92.9	377	2 T04213	heat shock transcr
33	52	92.9	378	2 S04336	U1 snRNP 70K prote
34	52	92.9	383	2 C96581	hypothetical prote
35	52	92.9	384	1 A26099	glycine-rich cell
36	52	92.9	385	2 S40778	ribonucleoprotein
37	52	92.9	395	2 S52423	protein kinase (EC
38	52	92.9	396	2 T49109	glycine-rich prote
39	52	92.9	404	2 S54729	RNA-binding protei
40	52	92.9	427	2 A32372	female-specific do
41	52	92.9	431	1 WJH2G	homeotic protein H
42	52	92.9	433	2 S20963	homeotic protein H
43	52	92.9	465	1 S01820	glycine-rich cell
44	52	92.9	475	2 A43915	homeotic protein e
45	52	92.9	490	2 T09084	phosphatidylinosit
46	52	92.9	508	2 S59870	fork head domain p
47	52	92.9	526	1 S33799	RNA-binding protei
48	52	92.9	528	2 G02127	fus-like protein -
49	52	92.9	528	2 D46449	hypothetical prote
50	52	92.9	531	2 S09859	hypothetical prote
51	52	92.9	543	2 A41211	early growth respo
52	52	92.9	549	2 B32372	male-specific doub
53	52	92.9	564	2 T49322	related to RNA-bin
54	52	92.9	587	1 B44276	coat protein VP1 -
55	52	92.9	594	2 B86456	protein trihelix D
56	52	92.9	600	2 T14613	hypothetical prote
57	52	92.9	603	2 T45671	ATP-dependent RNA
58	52	92.9	616	2 A58947	signal recognition
59	52	92.9	660	2 S24125	potassium channel
60	52	92.9	664	2 JC7990	acetylcholinestera
61	52	92.9	690	2 D98318	ABC protein AGR L
62	52	92.9	698	2 A54796	regulatory protein
63	52	92.9	716	1 VCPV2M	coat protein VP1 -
64	52	92.9	718	1 VCPVIM	coat protein VP1 -
65	52	92.9	722	1 VCPVV2	coat protein VP1 -
66	52	92.9	793	2 S59067	penton long fiber
67	52	92.9	877	2 T43449	hypothetical prote
68	52	92.9	892	2 T27005	hypothetical prote
69	52	92.9	895	2 JC7089	zinc finger bindin
70	52	92.9	979	2 A35913	regulatory factor
71	52	92.9	1090	2 A41696	regulatory protein
72	52	92.9	1102	2 JC6316	probable protein k
73	52	92.9	1226	2 T24045	hypothetical prote
74	52	92.9	1325	1 S73723	probable lipoprote
75	52	92.9	1532	2 A61262	collagen alpha 1(X
76	52	92.9	1969	2 T08875	histidine kinase h
77	52	92.9	2783	1 A41948	alpha-fetoprotein
78	52	92.9	3016	2 S77300	hypothetical prote
79	51	91.1	257	2 C84890	hypothetical prote
80	50	89.3	183	2 PNO109	keratin-like prote
81	50	89.3	214	1 KNN12S	glycine-rich prote
82	50	89.3	252	2 T03160	capsid protein - a
83	50	89.3	257	2 B84346	hypothetical prote
84	50	89.3	266	1 CIRBL	calpain (EC 3.4.22
85	50	89.3	284	2 S74256	homeotic protein s
86	50	89.3	286	2 A47318	RNA-binding protei
87	50	89.3	296	2 I53142	gene Merc protein
88	50	89.3	316	1 A38743	loricrin - human
89	50	89.3	320	2 G96714	hypothetical prote
90	50	89.3	330	2 S74255	homeotic protein s
91	50	89.3	382	2 E91083	hypothetical membr
92	50	89.3	382	2 P85928	hypothetical prote
93	50	89.3	387	2 S33312	dnaj protein - lee
94	50	89.3	418	2 S42031	LDJ2 protein - lee
95	50	89.3	441	2 T49265	hypothetical prote
96	50	89.3	466	2 A36674	transcription fact
97	50	89.3	468	1 A54258	transcription fact
98	50	89.3	473	2 S70357	forkhead transcrip
99	50	89.3	481	2 A36628	loricrin - mouse
100	50	89.3	495	2 B71360	hypothetical prote
101	50	89.3	639	2 A55719	dnak-type molecula
102	50	89.3	685	2 JC6331	rho-type guanine e

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:54:42 ; Search time 13.125 Seconds
(without alignments)
294.675 Million cell updates/sec

Title: US-10-622-108-28

Perfect score: 56

Sequence: 1 GGGSGGGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	3	AAY97238 Peptide 1
2	56	100.0	10	4	AAE06270 Glycine 1
3	56	100.0	10	4	AB81034 Linker pe
4	56	100.0	10	4	AAG77866 HLA adapt
5	56	100.0	10	4	AB31588 Linker us
6	56	100.0	10	5	ABP51822 Fusion pr
7	56	100.0	10	5	AAU82114 T-cell sp
8	56	100.0	10	5	AAE25958 Linker pe
9	56	100.0	10	5	AAE23160 Glycine-r
10	56	100.0	10	5	AAE13619 Peptide 1
11	56	100.0	10	6	AAO26601 Fusion pr
12	56	100.0	10	6	ABP56233 Single ch
13	56	100.0	10	6	ABJ26727 VEGF bind
14	56	100.0	10	6	ABG72090 PUC19-42K
15	56	100.0	10	6	ABU55753 Polylinke
16	56	100.0	10	6	AAE37749 Linker pe
17	56	100.0	10	7	ADC34708 (Gly4Ser)
18	56	100.0	10	7	ADF69795 M. tuberc
19	56	100.0	10	7	ADF11030 Peptide 1
20	56	100.0	10	7	ADG32335 Peptide 1
21	56	100.0	10	7	ADH73607 Spacer pe
22	56	100.0	10	7	AD140259 Linker pe
23	56	100.0	10	7	AD106621 stNFR1:lg
24	56	100.0	10	7	AD106630 hutNFR:lg
25	56	100.0	10	7	ADS19142 Peptide 8

26	56	100.0	10	8	ADG47240	Adg47240 Peptide u
27	56	100.0	10	8	ADI82602	Adi82602 Fab elbow
28	56	100.0	10	8	ADK18213	Adk18213 Mouse ant
29	56	100.0	10	8	ADL23305	Adl23305 Linker pe
30	56	100.0	10	8	ADL24299	Adl24299 Cardiovas
31	56	100.0	10	8	ADM98278	Adm98278 (Gly4Ser)
32	56	100.0	10	8	ADO21839	Ado21839 Histone a
33	56	100.0	10	8	ADQ59569	Adq59569 Protein f
34	56	100.0	10	8	ADR32306	Adr32306 Linker pe
35	56	100.0	11	2	AAE99242	AAE99242 (Gly4Ser)
36	56	100.0	12	3	AB25906	Ab25906 Linker se
37	56	100.0	12	5	AAU82047	AAU82047 T-cell sp
38	56	100.0	12	6	ABU09673	ABU09673 INF-beta-
39	56	100.0	12	6	ABP72704	ABP72704 Flexible
40	56	100.0	13	2	AAE43499	AAE43499 Linker fo
41	56	100.0	13	3	AB29543	Ab29543 Linker pe
42	56	100.0	13	3	AAE44696	AAE44696 Peptide 1
43	56	100.0	13	3	AAE80115	AAE80115 IL-6R and
44	56	100.0	13	3	AAE83213	AAE83213 Peptide 1
45	56	100.0	13	3	AAE83220	AAE83220 Peptide 1
46	56	100.0	13	4	AB81897	Ab81897 IL6 recep
47	56	100.0	13	6	ABP72701	ABP72701 Flexible
48	56	100.0	14	2	AAE87024	AAE87024 Flexible
49	56	100.0	14	2	AAW23417	AAW23417 Linker pe
50	56	100.0	14	2	AAW47355	AAW47355 Polylinke
51	56	100.0	14	2	AAE17953	AAE17953 Amino aci
52	56	100.0	14	2	AAE27115	AAE27115 Linker pe
53	56	100.0	14	2	AAE23638	AAE23638 Linker pe
54	56	100.0	14	3	AB03812	AB03812 Polylinke
55	56	100.0	14	3	AAE99938	AAE99938 Peptide u
56	56	100.0	14	4	AAE62063	AAE62063 Sequence
57	56	100.0	14	4	AAE72751	AAE72751 Poly link
58	56	100.0	14	4	AB56483	AB56483 Human sin
59	56	100.0	14	6	ABP70843	ABP70843 Linker pe
60	56	100.0	14	6	AAE37748	AAE37748 Linker pe
61	56	100.0	14	8	ADI47373	ADI47373 Plasmid p
62	56	100.0	14	8	ADJ88260	ADJ88260 Polylinke
63	56	100.0	14	8	ADO49278	ADO49278 Peptide 1
64	56	100.0	14	8	ADO49266	ADO49266 Peptide 1
65	56	100.0	14	8	ADQ91247	ADQ91247 Interleuk
66	56	100.0	14	8	ADR01303	ADR01303 Polylinke
67	56	100.0	15	2	AAE25983	AAE25983 Peptide m
68	56	100.0	15	2	AAE59501	AAE59501 Hydrophil
69	56	100.0	15	2	AAE59500	AAE59500 Hydrophil
70	56	100.0	15	2	AAE85123	AAE85123 Gene deli
71	56	100.0	15	2	AAE76583	AAE76583 Human ONS
72	56	100.0	15	2	AAE99244	AAE99244 (Gly4Ser)
73	56	100.0	15	2	AAE95067	AAE95067 scFv spac
74	56	100.0	15	2	AAE09323	AAE09323 Peptide 1
75	56	100.0	15	2	AAE49219	AAE49219 Sequence
76	56	100.0	15	2	AAE10295	AAE10295 Peptide 1
77	56	100.0	15	2	AAE35984	AAE35984 Peptide 1
78	56	100.0	15	2	ABE76199	ABE76199 Anti-meso
79	56	100.0	15	2	AAE87784	AAE87784 Antibody-
80	56	100.0	15	2	AAE43414	AAE43414 Peptide S
81	56	100.0	15	2	AAE33328	AAE33328 E6-sFv pe
82	56	100.0	15	2	AAE03763	AAE03763 Linker pe
83	56	100.0	15	2	AAE21600	AAE21600 EP-919566
84	56	100.0	15	2	AAE27397	AAE27397 Flexible
85	56	100.0	15	3	AAE16564	AAE16564 Peptide 1
86	56	100.0	15	3	AAE29542	AAE29542 Linker pe
87	56	100.0	15	3	AAE99636	AAE99636 (gly4ser)
88	56	100.0	15	3	AB22838	AB22838 Single ch
89	56	100.0	15	3	AAE70606	AAE70606 Protein e
90	56	100.0	15	3	AAE79551	AAE79551 Linker pe
91	56	100.0	15	3	AAE79552	AAE79552 Linker pe
92	56	100.0	15	3	AAE90826	AAE90826 Linker am
93	56	100.0	15	3	AB23816	AB23816 Plasmid p
94	56	100.0	15	3	AAE97237	AAE97237 Peptide 1
95	56	100.0	15	4	AB15682	AB15682 Single-ch
96	56	100.0	15	4	AB70169	AB70169 Gly/Ser 1
97	56	100.0	15	4	AB98920	AB98920 Linker pe
98	56	100.0	15	4	AAE13082	AAE13082 Glycine 1

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:54:42 ; Search time 297.938 Seconds
(without alignments)
294.675 Million cell updates/sec

Title: US-10-622-108-2
Perfect score: 1233
Sequence: 1 DKHTTCPPCPAPELIGPSV.....MHEALNNHYTKSLSLSPGK 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

```
Database : A_Geneseq_16Dec04:
1: Geneseq1380s:
2: Geneseq1390s:
3: Geneseq1390s:
4: Geneseq2000s:
5: Geneseq2001s:
6: Geneseq2002s:
7: Geneseq2003as:
8: Geneseq2003bs:
9: Geneseq2004s:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1233	100.0	227	7	ADD31433	Add31433 And
2	1233	100.0	227	7	ADU64196	Adu64196 Hun
3	1233	100.0	227	7	ADK82704	Adk82704 Hun
4	1233	100.0	227	8	ADO10505	Ado10505 Hun
5	1233	100.0	227	8	ADL92470	Adl92470 Hun
6	1233	100.0	227	8	ADQ11815	Adq11815 Hun
7	1233	100.0	228	3	AAI96529	Aay96529 Hun
8	1233	100.0	228	3	AAI16955	Aab16955 Hun
9	1233	100.0	228	4	AAB39893	Aab39893 Hun
10	1233	100.0	228	5	ABB04279	Abb04279 Hun
11	1233	100.0	228	5	AAU81074	Aau81074 Hun
12	1233	100.0	228	5	AAE34310	Aae14310 Hun
13	1233	100.0	228	5	ABB73410	Abb73410 Hun
14	1233	100.0	228	5	AAE66012	Aae66012 Hun
15	1233	100.0	228	5	AAU73018	Aau73018 Hun
16	1233	100.0	228	6	ABT38267	Abt38267 Hun
17	1233	100.0	228	7	ADN59683	Adn59683 Hun
18	1233	100.0	228	8	ADM17708	Adm17708 Hun
19	1233	100.0	228	8	ADG75523	Adg75523 Hun
20	1233	100.0	228	6	ABD39450	Abd39450 Hun
21	1233	100.0	228	6	ABD39450	Abd39450 Hun
22	1233	100.0	228	6	ABD39450	Abd39450 Hun
23	1233	100.0	232	2	AAW53522	Aaw53522 Hun
24	1233	100.0	232	3	AAE28690	Aae28690 Hun
25	1233	100.0	232	4	AAE80897	Aae80897 Hun

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OM protein - protein search, using sw model
Run on: September 19, 2005, 08:58:27 ; Search time 56.75 Seconds
(without alignments)
384.867 Million cell updates/sec

Title: US-10-622-108-2
Perfect score: 1233
Sequence: 1 DKHTCPCPAPELLGQPSV.....MHEALHHYTKSLSLSPGK 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	100.0	255	4	S31866
2	1233	100.0	330	1	GHHU
3	1227	99.5	374	2	S69339
4	1180	95.7	234	2	PT0207
5	1146	92.9	377	2	A23511
6	1144	92.8	377	2	A60764
7	1142.5	92.7	326	1	G2HU
8	1135	92.1	327	1	G4HU
9	1121	90.9	289	1	G3HUWI
10	917.5	74.4	323	1	GHRB
11	906.5	73.5	328	2	I47160
12	906.5	73.5	328	2	I47159
13	903	73.2	277	2	I47162
14	889	72.1	329	1	G2GP
15	885.5	71.8	328	2	I47158
16	878.5	71.2	328	2	I47161
17	855.5	69.4	470	2	S22080
18	846	68.6	308	2	C30554
19	846	68.6	472	2	S31459
20	845.5	68.6	329	1	G3MSC
21	838	68.0	333	2	PS0018
22	834.5	67.7	398	1	G3MSM
23	827.5	67.1	444	2	PC4436
24	818.5	66.4	326	2	PS0017
25	817.5	66.3	324	1	G1MS
26	812.5	65.9	393	1	G1MSM
27	809.5	65.7	329	2	S00847
28	809	65.6	330	1	G2MSA
29	809	65.6	469	2	S37483

30	804	65.2	399	1	G2MSAM	Ig gamma-2a chain
31	802	65.0	335	1	G2MSAB	Ig gamma-2a chain
32	794	64.4	446	2	S40295	Ig gamma-2a chain
33	785.5	63.7	322	2	PS0019	Ig gamma-2a chain
34	779	63.2	474	1	G2MS11	Ig gamma-2b chain
35	774	62.8	405	1	G2MSBM	Ig gamma-2b chain
36	764	62.0	327	2	S06611	Ig gamma-2 chain C
37	757	61.4	475	2	S01321	Ig gamma-2b chain
38	707	57.3	180	2	I46732	Ig gamma heavy chain
39	577.5	46.8	249	2	S69340	Ig heavy chain VHI
40	574.5	46.6	218	2	A36040	Ig heavy chain V-I
41	571	46.3	152	2	S14236	Ig gamma-1 chain C
42	395.5	32.1	572	2	B46529	Ig Y heavy chain (
43	358	29.0	343	2	S25644	Ig mu chain C regi
44	358	29.0	453	2	S37768	Ig mu chain C regi
45	357.5	29.0	549	2	S04845	Ig heavy chain pre
46	357	29.0	455	1	MHMS	Ig mu chain C regi
47	357	29.0	455	2	A24976	Ig heavy chain C r
48	356.5	28.9	448	2	S03186	Ig mu heavy chain
49	356	28.9	391	1	MHHUBT	Ig epsilon chain C
50	354	28.7	388	1	EHMS	Ig epsilon chain C
51	353	28.6	426	2	I36948	Ig epsilon chain -
52	353	28.6	429	1	EHRT	Ig epsilon chain C
53	352	28.5	428	1	EHHU	Ig epsilon chain C
54	351	28.5	548	2	S38864	Ig epsilon chain C
55	349.5	28.3	452	1	MGHU	Ig mu chain C regi
56	348	28.2	627	2	S14683	Ig mu chain precu
57	347	28.1	476	1	MHMSM	Ig mu chain C regi
58	345	28.0	474	2	S15590	Ig heavy chain - h
59	342	27.7	458	1	MHRB	Ig mu chain C regi
60	342	27.7	504	2	S00390	Ig gamma chain (cl
61	339.5	27.5	473	1	MHHUM	Ig mu chain C regi
62	335	27.2	454	1	MHHY	Ig mu chain C regi
63	333	27.0	423	1	EHMS	Ig epsilon chain C
64	332	26.9	450	1	MHDG	Ig mu chain C regi
65	332	26.9	479	1	MHRBM	Ig mu chain C regi
66	331.5	26.9	112	2	B30503	Ig gamma-2a chain
67	329	26.7	457	2	S03961	Ig mu chain C regi
68	327	26.5	592	2	S25705	Ig mu chain - shae
69	316	25.6	453	2	C31933	Ig mu chain C regi
70	306	24.8	433	2	S31436	Ig upsilon chain -
71	299.5	24.3	357	2	S09269	Ig alpha chain C r
72	298	24.2	577	2	I50731	Ig heavy chain - n
73	297	24.1	438	1	HVRKC2	Ig mu chain C regi
74	295.5	24.0	299	1	AHRB	Ig alpha chain C r
75	294	23.8	342	2	I47175	Ig alpha chain C r
76	291	23.6	357	2	S09265	Ig alpha chain C r
77	289.5	23.5	338	2	S09276	Ig mu chain C regi
78	287.5	23.3	367	1	MHCH	Ig mu chain C regi
79	287.5	23.3	438	1	HVRKCS	Ig alpha chain C r
80	285.5	23.2	343	2	S09272	Ig mu chain C regi
81	278.5	22.6	461	1	HVRKCO	Ig alpha chain C r
82	277	22.5	339	2	S09264	Ig mu chain C regi
83	276.5	22.4	393	1	HVRKCI	Ig gamma-2b chain
84	275.5	22.3	88	2	A30503	Ig alpha chain C r
85	275.5	22.3	352	2	S09266	Ig alpha chain C r
86	275	22.3	585	2	A46507	Ig alpha chain C r
87	272.5	22.1	357	2	S09267	Ig alpha chain C r
88	272.5	22.1	684	2	S60266	novel antigen rece
89	272	22.1	353	1	A1HU	Ig alpha-1 chain C
90	272	22.1	370	1	HVRKCS	Ig mu chain C regi
91	267.5	21.7	244	2	I2328	Ig heavy chain C r
92	267.5	21.7	348	2	S09270	Ig alpha chain C r
93	267.5	21.7	352	2	S05500	Ig alpha-1 chain C
94	267	21.7	340	2	B23360	Ig alpha-2 chain C
95	266.5	21.6	348	2	S09273	Ig alpha chain C r
96	265	21.5	360	2	S09271	Ig alpha chain C r
97	264.5	21.5	347	2	S09274	Ig alpha chain C r
98	264	21.4	340	2	I56230	Ig alpha-2 chain -
99	262	21.2	111	2	S43148	Ig upsilon chain -
100	260.5	21.1	358	2	S09268	Ig alpha chain C r
101	255.5	20.7	342	2	A45966	Ig alpha chain C r
102	255	20.7	340	1	A2HU	Ig alpha-2 chain C

Sample No.	Score	Query			ID	Description
		Match	Length	DB		
1228	100.0	227	15	US-10-269-695-60	Sequence 60, Appl	
1229	100.0	227	15	US-10-435-608-2	Sequence 2, Appl	
1230	100.0	227	15	US-10-410-998-60	Sequence 60, Appl	
1231	100.0	227	15	US-10-622-108-2	Sequence 2, Appl	
1232	100.0	227	16	US-10-742-379-296	Sequence 296, App	
1233	100.0	227	17	US-10-822-231-2	Sequence 2, Appl	
1234	100.0	228	9	US-09-847-712-2	Sequence 2, Appl	
1235	100.0	228	9	US-09-840-717-2	Sequence 2, Appl	
1236	100.0	228	10	US-09-847-249A-2	Sequence 2, Appl	
1237	100.0	228	10	US-09-843-221A-2	Sequence 2, Appl	
1238	100.0	228	10	US-09-840-569B-2	Sequence 2, Appl	

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:57:42 ; Search time 270.397 Seconds
(without alignments)
429.894 Million cell updates/sec

Title: US-10-622-108-2

Perfect score: 1233

Sequence: 1 DKHTCCPPCAPPELLGGPSV.....MHEALHNHYTKSLSPGK 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	100.0	330	1	GC1_HUMAN
2	1233	100.0	465	2	Q6GMX6
3	1233	100.0	466	2	Q6IN78
4	1233	100.0	469	2	Q7Z7P5
5	1233	100.0	470	2	Q6FJA4
6	1233	100.0	470	2	Q7Z5W1
7	1233	100.0	472	2	Q6N089
8	1233	100.0	475	2	Q6GMW7
9	1233	100.0	475	2	Q6GMX1
10	1233	100.0	679	2	Q6PQ8
11	1229	99.7	473	2	Q6P055
12	1229	99.7	475	2	Q6MZ06
13	1229	99.7	480	2	Q6N094
14	1229	99.7	481	2	Q6N097
15	1229	99.7	482	2	Q7Z351
16	1227	99.5	348	2	Q6PYX1
17	1227	99.5	473	2	Q6M2V7
18	1227	99.5	478	2	Q6P181
19	1227	99.5	480	2	Q6PJF1
20	1226	99.4	466	2	Q6N096
21	1222	99.1	475	2	Q6N095
22	1222	99.1	544	2	Q6PJ95
23	1216	98.6	487	2	Q6SZL2
24	1146	92.9	354	2	Q6ET72
25	1146	92.9	518	2	Q6N030
26	1142.5	92.7	326	1	GC2_HUMAN
27	1142.5	92.7	417	2	Q6N093
28	1142	92.6	521	2	Q6N4Y9
29	1139.5	92.4	464	2	Q6MZ06
30	1137.5	92.3	465	2	Q6P6C4
31	1135	92.1	327	1	GC4_HUMAN

32	1135	92.1	473	2	Q8TC63	Q8TC63 homo sapien
33	1131	91.7	509	2	Q8NF17	Q8NF17 homo sapien
34	1128.5	91.5	493	2	Q68CN4	Q68CN4 homo sapien
35	1126	91.3	290	1	GC3_HUMAN	P01860 homo sapien
36	1126	91.3	476	2	Q6MZX7	Q6MZX7 homo sapien
37	917.5	74.4	323	1	GC_RABIT	P01870 oryctolagus
38	909	73.7	337	2	Q95M34	P01862 equus caball
39	889	72.1	329	1	GC2_CAVPO	P01862 cavia porce
40	845.5	68.6	329	1	GC3_MOUSE	P22436 mus musculus
41	845.5	68.6	470	2	Q7TMK1	Q7TMK1 mus musculus
42	838	68.0	333	1	GC_RAT	P20761 rattus norv
43	834.5	67.7	303	2	Q6KAM2	Q6KAM2 mus musculus
44	834.5	67.7	398	1	GC3M_MOUSE	P03987 mus musculus
45	828.5	67.2	463	2	Q99LC4	Q99LC4 mus musculus
46	827.5	67.1	458	2	Q65ZQ1	Q65ZQ1 homo sapien
47	818.5	66.4	326	1	GC1_RAT	P20759 rattus norv
48	817.5	66.3	324	1	GC1_MOUSE	P01868 mus musculus
49	812.5	65.9	393	1	GC1N_MOUSE	P01869 mus musculus
50	811	65.8	473	2	Q9D8L4	Q9D8L4 mus musculus
51	809.5	65.7	329	1	GC_RAT	P20762 rattus norv
52	809	65.6	330	1	GCAA_MOUSE	P01863 mus musculus
53	809	65.6	464	2	Q6PF95	Q6PF95 mus musculus
54	805	65.3	464	2	Q6PIB8	Q6PIB8 mus musculus
55	805	65.3	465	2	Q6FJB2	Q6FJB2 mus musculus
56	805	65.3	471	2	Q66K04	Q66K04 mus musculus
57	805	65.3	472	2	Q6PJA7	Q6PJA7 mus musculus
58	804	65.2	399	1	GCAM_MOUSE	P01865 mus musculus
59	802	65.0	335	1	GCAB_MOUSE	P01864 mus musculus
60	785.5	63.7	322	1	GC_RAT	P20760 rattus norv
61	780	63.3	473	2	Q91Z05	Q91Z05 mus musculus
62	780	63.3	474	2	Q8R3H6	Q8R3H6 mus musculus
63	779	63.2	336	1	GCB_MOUSE	P01866 mus musculus
64	774	62.8	405	1	Q86TT1	Q86TT1 homo sapien
65	358	29.0	375	2	Q86TT1	Q86TT1 homo sapien
66	358	29.0	454	1	MUC_HUMAN	P01871 homo sapien
67	358	29.0	597	2	Q96BB9	Q96BB9 homo sapien
68	358	29.0	597	2	Q6GMX5	Q6GMX5 homo sapien
69	358	29.0	597	2	Q9BQB8	Q9BQB8 homo sapien
70	358	29.0	597	2	Q9BU10	Q9BU10 homo sapien
71	358	29.0	606	2	Q6GMV2	Q6GMV2 homo sapien
72	357	29.0	455	1	MUC_MOUSE	P01872 mus musculus
73	356	28.9	391	1	MUCB_HUMAN	P04220 homo sapien
74	355.5	28.8	585	2	Q6GPX4	Q6GPX4 xenopus lae
75	354	28.7	421	1	BPC_MOUSE	P06336 mus musculus
76	353	28.6	429	1	BPC_RAT	P01855 rattus norv
77	352	28.5	428	1	BPC_HUMAN	P01854 homo sapien
78	349.5	28.3	584	2	Q6INK3	Q6INK3 xenopus lae
79	349	28.3	614	2	Q7TMT6	Q7TMT6 mus musculus
80	348	28.2	595	2	Q8WUX4	Q8WUX4 homo sapien
81	348	28.2	613	2	Q8WUX1	Q8WUX1 homo sapien
82	348	28.2	620	2	Q96EY0	Q96EY0 homo sapien
83	348	28.2	625	2	Q96AA6	Q96AA6 homo sapien
84	347	28.1	476	1	MUCM_MOUSE	P01873 mus musculus
85	347	28.1	613	2	Q8VCX7	Q8VCX7 mus musculus
86	342	27.9	458	1	MUC_RABIT	P03988 oryctolagus
87	342	27.9	450	1	MUC_CANTA	P01874 canis famil
88	332	26.9	454	1	MUC_MESAU	P06337 mesocricetu
89	332	26.9	479	1	MUCM_RABIT	P04221 oryctolagus
90	329	26.7	457	1	MUC_SUNMU	P20768 suncus muri
91	319	25.9	572	2	Q66IQ7	Q66IQ7 xenopus lae
92	316	25.6	587	2	Q7TOR1	Q7TOR1 xenopus lae
93	316	25.6	588	2	Q6IR66	Q6IR66 xenopus lae
94	316	25.6	593	2	Q6INM5	Q6INM5 xenopus lae
95	316	25.6	605	2	Q6GN83	Q6GN83 xenopus lae
96	310	25.1	614	2	Q6DDQ7	Q6DDQ7 xenopus lae
97	297	24.1	438	1	HVC2_HETFR	P23085 heterodontu
98	295.5	24.0	299	1	ALC_RABIT	P01879 oryctolagus
99	287.5	23.3	438	1	HVC5_HETFR	P23087 heterodontu
100	287.5	23.3	446	1	MUC_CHICK	P01875 gallus gall
101	278.5	22.6	461	1	HVCN_HETFR	P23088 heterodontu
102	276.5	22.4	393	1	HVC3_HETFR	P23086 heterodontu
103	272.5	22.1	684	2	Q90544	Q90544 ginglymoeto
104	272	22.1	353	1	ALC1_HUMAN	P01876 homo sapien

(FILE 'HOME' ENTERED AT 09:41:22 ON 09 SEP 2005)

FILE 'MEDLINE' ENTERED AT 09:41:27 ON 09 SEP 2005

L1 8863 SEA PLU=ON INTEFERON ALPHA OR IFN ALPHA

L2 2 SEA PLU=ON L1 AND (FUSE OR FUSED OR FUSION) AND
(IMMUNOGLOBULI
N OR ANTIBODY) AND HEAVY CHAIN
D BIB AB 1 2

FILE 'STNGUIDE' ENTERED AT 09:43:31 ON 09 SEP 2005

FILE 'CAPLUS, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH' ENTERED
AT 09:47:48

ON 09 SEP 2005

L3 8 SEA PLU=ON L2

Art Unit: 1635

L4 5 DUP REM L3 (3 DUPLICATES REMOVED)
D BIB AB 1-5

FILE 'STNGUIDE' ENTERED AT 09:53:57 ON 09 SEP 2005

(FILE 'HOME' ENTERED AT 10:44:47 ON 09 SEP 2005)

FILE 'MEDLINE' ENTERED AT 10:44:53 ON 09 SEP 2005

L1 19461 SEA PLU=ON INTERFERON ALPHA OR IFN ALPHA
L2 16 SEA PLU=ON L1 AND AEROSOL
D TI 1-16
L3 2 SEA PLU=ON L2 AND SYSTEMIC
D BIB AB 1 2
L4 80 SEA PLU=ON (IMMUNOGLOBULIN OR FC) AND AEROSOL?
AND SYSTEMIC
D TI 40-80
L5 9 SEA PLU=ON AEROSOL (5A) (IMMUNOGLOBULIN OR FC)
D TI 1-9
L6 21 SEA PLU=ON AEROSOL? (5A) (IMMUNOGLOBULIN OR FC)
D TI 1-21
D BIB AB 1 13 15-17

FILE 'STNGUIDE' ENTERED AT 10:53:43 ON 09 SEP 2005

FILE 'MEDLINE' ENTERED AT 11:02:45 ON 09 SEP 2005

L7 12 SEA PLU=ON INTERFERON ALPHA AND EFFECTIVE DOSE
D TI 1-12
D BIB AB 9 6 2 1

FILE 'MEDLINE' ENTERED AT 11:09:16 ON 09 SEP 2005

L8 80 SEA PLU=ON L1 AND NEOPTERIN
L9 0 SEA PLU=ON L8 AND OLIGOADENYLATE SYNTHASE
L10 425 SEA PLU=ON L1 AND (OLIGOADENYLATE SYNTHASE OR
OLIGOADENYLATE
SYNTHETASE OR OLIGO ADENYLATE SYNTHETASE OR OLIGO
ADENYLATE
SYNTHASE)
L11 9 SEA PLU=ON L10 AND NEOPTERIN
D TI 1-9
D BIB AB 1-9

FILE 'STNGUIDE' ENTERED AT 11:15:35 ON 09 SEP 2005

Art Unit: 1635

(FILE 'HOME' ENTERED AT 12:26:28 ON 09 SEP 2005)

FILE 'MEDLINE' ENTERED AT 12:26:36 ON 09 SEP 2005

L1 103 SEA PLU=ON LUNG ZONE DEPOSITION RATIO OR
PENETRATION INDEX
L2 51 SEA PLU=ON PENETRATION INDEX AND LUNG
L3 0 SEA PLU=ON LUNG ZONE DEPOSITION RATIO
L4 41 SEA PLU=ON L2 AND AEROSOL?
D TI 1-41

FILE 'STNGUIDE' ENTERED AT 12:28:28 ON 09 SEP 2005

FILE 'MEDLINE' ENTERED AT 12:34:48 ON 09 SEP 2005

L5 0 SEA PLU=ON ?GGGGSGGGS?

FILE 'CAPLUS, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH' ENTERED
AT 12:35:29

ON 09 SEP 2005

L6 0 SEA PLU=ON L5
L7 0 SEA PLU=ON GGGGSGGGS?

(FILE 'HOME' ENTERED AT 10:25:11 ON 10 NOV 2005)

FILE 'MEDLINE' ENTERED AT 10:25:23 ON 10 NOV 2005

L1 19944 SEA PLU=ON (INTERFERON ALPHA OR IFN ALPHA OR
IFNALPHA OR
IFNA)
L2 881 SEA PLU=ON L1 AND RECEPTOR AND TUMOR
L3 42 SEA PLU=ON L2 AND OVEREXPRESS?
D TI 1-42
D BIB AB 33 26 20 15
L4 198 SEA PLU=ON L1 AND OVEREXPRESS?
L5 51 SEA PLU=ON L4 AND (CANCER OR NE0PLAS? OR
CARCINOMA)
L6 2 SEA PLU=ON L5 AND RECEPTOR (3A) (INTERFERON ALPHA
OR IFN
ALPHA OR IFNALPHA OR IFNA)
D BIB AB 1 2

FILE 'STNGUIDE' ENTERED AT 10:34:22 ON 10 NOV 2005

FILE 'MEDLINE' ENTERED AT 10:35:00 ON 10 NOV 2005

Art Unit: 1635

L7 693 SEA PLU=ON RECEPTOR (3A)L1
L8 91 SEA PLU=ON L7 AND (T CELL OR B CELL)
L9 5 SEA PLU=ON L8 AND LYMPHOMA
D BIB AB 105

FILE 'STNGUIDE' ENTERED AT 10:38:04 ON 10 NOV 2005

FILE 'STNGUIDE' ENTERED AT 10:44:09 ON 10 NOV 2005

FILE 'MEDLINE' ENTERED AT 10:46:52 ON 10 NOV 2005

L10 10 SEA PLU=ON (IFN-ALPHA 2B OR IFNA2B OR IFNALPHA2B OR
IFN A2B
OR INTERFERON A2B OR INTERFEREON ALPHA2B OR
INTERFERON ALPHA
2B) (3A) RECEPTOR
D TI 1-10
D BIB AB 10 8 7 6 5 4

FILE 'STNGUIDE' ENTERED AT 10:50:54 ON 10 NOV 2005

L11 0 SEA PLU=ON (AEROSOL OR LUNG OR INHAL?) AND (IFN-
ALPHA 2B OR
IFNA2B OR IFNALPHA2B OR IFN A2B OR INTERFERON A2B OR
INTERFEREO
N ALPHA2B OR INTERFERON ALPHA 2B)

FILE 'MEDLINE' ENTERED AT 11:02:53 ON 10 NOV 2005

L12 57 SEA PLU=ON (AEROSOL OR LUNG OR INHAL?) AND (IFN-
ALPHA 2B OR
IFNA2B OR IFNALPHA2B OR IFN A2B OR INTERFERON A2B OR
INTERFEREO
N ALPHA2B OR INTERFERON ALPHA 2B)

D TI 1-57

D BIB AB 50 54 52 51

L13 3 SEA PLU=ON L12 NOT LUNG

D BIB AB 1-3

L14 3 SEA PLU=ON L12 AND (AEROSOL? OR INHAL?)

(FILE 'HOME' ENTERED AT 12:54:54 ON 10 NOV 2005)

FILE 'MEDLINE' ENTERED AT 12:55:22 ON 10 NOV 2005

L1 1141 SEA PLU=ON (IFNA2B OR IFNA 2B OR IFN A2B OR IFN A 2B
OR

Art Unit: 1635

INTERFEREON ALPHA2B OR INTERFERON ALPHA 2B OR
INTERFERON ALPHA

2 B)

L2 36 SEA PLU=ON L1 AND LYMPHOMA
D TI 1-36

D BIB AB 35 34 33 32 31 30 23 22 21

L3 0 SEA PLU=ON L1 AND AEROSOL?

L4 1 SEA PLU=ON L1 AND LYMPHOMA AND APOPTO?
D BIB AB

~~This system removes particles of greater than about 4 of a therapeutically~~
effective dose of a therapeutically active growth factor having a molecular weight of
about **5 to 75 kD**, said method comprising administering to said patient by inhalation,